## SEARCH REQUEST FORM

Requestor's

Serial

Name:	Number:			
Date: Phone	e:	Art Unit:		
Search Topic: Please write a detailed statement of search topic. Describe that may have a special meaning. Give examples or relevar a copy of the sequence. You may include a copy of the b	ni citations, authors keywords,	etc., if known. For sequence:	efine any terms s, please attach	100mm 1971年 日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の日本の日
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Gentore warsion 5.1.3 Copyright (c) 1953 - 2002 Compugen Ltd.	OW nucleic - nucleic search, using sw model	Nun on: November 1, 2002, 22:58:32 ; Search time 2426 Seconds (villoute alignment) (villoute alignment) (1) (villoute) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1	Title: US-09-720-384A-3 Perfect score: 1217 Squedence: 1217 Squedence: 1227 Sq	Scoring table: IDBWTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1797656 seqs, 10463268293 residues	Code induced to Little Section and Code Managements: 3595312 Minimum DB Seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Maximum Maximum Alasting first 45 summaries	popopopopo		2.2 ent.ov: - 2.2 ent.ov: - 2.3 ent.ov: - 2.5 ent.ov: - 2.		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Down: To Score Asach Lampth 19 ID Description

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Location/Qualifiers
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/note="APS kinase; ATP adenosine-5'-phosphosulfate
3'-phosphotransferase"
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/product="adenosine-5'-phosphosuifate kinase"
/protein_id="AARI7236.1"
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Arabidopsis thallana Ar4938940/T5J17_110 mRRA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thalians in tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Midiplantee; Streptophyta; Spermatophyta; Magnollophyta; Addiocyladons; core enditors; Cabaidae; eurosida II; Brassloaks; Mrassloaceae; Arabidopels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRIEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI CONNe (RAFI CONN - KRIEN Arabidopes Pull-Length CONN ): Seki, N., Narrusaka, N., 18hida, J., 18ki, Saru, N., Kama, A., 18ki, Saru, T., Carninci, P., Kawai, J., 18hida, J., 18hida, J., Carninci, P., Kawai, J., 18hida, J., 18h
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                   651 CAGAAGACCGTGCAGAAATATACGAAGAGTGGTGAAGTGGCAAAGCTTTTTGCTGATG 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1011 AAAACGGATATTTGCAAGCTTAGTATGTAT 1042
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Arz.H.E., odsselmano, G., schlämenn, S. and Schwenn, J.D.
Dobna for adenylyl sulphase (Ars): Lianse from Archidopsis thallana
84.0chim. Blophys. Acta 1218 (3), 447-452 (1994)
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RYGEWSTKARANG I I CIASLI SEP REPREDACESLILPEGERF WEIGHTGORGERED IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="ATP:adenylylsulfate=3".phosphotransferase"
/PC number="2,7.1.25"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-NOV-1993) Schwenn J. D., Ruhr University Bochum, Biology, Universitaetsstr. 150, 44780 Bochum, Germany
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                                                                                                                                                                                               2 (Dases 1 to 1185)
Arz.H.E., Gisselmann,G., Schlffmann,S. and Schwenn,J.D.
A Chicorplate APS-Kinase CDNA from Arabidopsis thaliana
Umpublished
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/tissue_type="leaf"
/clone_lib="cDNa in lambda ZapII"
/dev_stage="vegetative"
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/db_xref="taxon:3702"
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/protein_id="CAA53426.1"
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A CANA Condensor, S. Schiffmann, S. and Schwenn, J. D. A CANA Condensor, Sulphase (ASS)-kinase from Arabidopsis thallane alochies. Biophys. Acta 1218 (3), 447-452 (1994).
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/protein_id="AAG39530.1"
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/VD_xxef=01808752314
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Requesting and another for the RAVE, OWDER cheek R., Chen H.,
KEIN, C.J., MORDER, M.C., STIAIR, P., BRANL, J. BOWSET, L., Dalado, J. K.,
KEIN, C.J., MORDER, M.C., STIAIR, P., BRANL, J. BOWSET, L., Dalado, J. K.,
KEIN, C.J., Chang, T., And Chang, T., KEIL, MORDER, C., Lean, B.,
Ralle, C.J., Dannie, P., K. Loberto, H. Land, Scatter, Rept. Prop. Proc. Pro
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Pred. No. 4.3e-52;
0; Mismatches 209; Indels 3;
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/db_xref="taxon:3702"
/cbromosome="4"
/clone="RAFL09-09-101(R21470)"
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Childress D., Zeng, C., and Smith.D.R.
Single Man and M DNYKGLIKKIGTG NE'NSVLTKIONGDNDNOYELKAGLNKRKDIRADIIDSLDRLM BDRINGETEERKLIJKTERSSIVVLLERPVITLLKSPFTDIADENKRILMUTDRI POSEAVARKKRREDELGYLLKVYDFGROLDIIKNILLKSGROENENKYNSKE TGL/GGTT-LISKAMA (THE LIST) AND THE TIST STATE THE TISTER THE THE TISTER THE /CTGRSIALION-"MRROSMGFIRNFTIRSKLLSLLLINVLLIVIVLFWIEIRARYS KKRGDINSVYCYNEKVINSLKDDLGISQDYIVQYVYDRNTHEYSKVELDRRIDKVKHL GFET PGEVTRII EDSYKNINTLYSRAY AQSMKYSKEIK REFSII SDKIRLFTEKSYNSY NNT REI IDKLODER PER DALIN RACKLYKE RUFNSYREID IEL RINK YSRENGEPULT NVDY IFFETWEVILDBERKYWKSIEDEI PKOLIL (SSWMITBEDLKOTYMDKELTAISQO /db\_xref="d1:15022927" Franslation="MRSTRLHOWNLEWTGATWUPIYMSNAYAHSSPOELEMVFKG KFYFTANSLRSPSWPTW-FBERRAAFIEGGLTATSAASCHSAIYMAITMIYHPEDELIAS /Eranslation-"MELSHDILKTDLLIVGGSTAGCFAAISAANKPSIHILIVEKFNI KRSGCLAAGVNALNAYITKNETPESEVDYVKKEFNEVVREDLIYTAAKRLNRVTEKVE /Lenslation-"mnnkkstnvvwqefkikronrekmikokgavimfyglsgsgkst vasalekkiyemgyilylidgdniryglnsdigfksedktenirrvsevakifadagi TTTTTSPFIEDRNARKLLGKDFVEVY IDCPIEVCEKRDPKGIYKKARNGEIKNFT KMGLTILKNEAGEYVSRGKRSIKINGENIKPILVDALKKKENIEVLNGVNIVDYIVRD /product-"AdenylyJsulfate reductase, subunit A" /Protein\_id="AAK78089.]" /db\_xref="GI:15022929" Pproduct\*"Methyl-accepting chemotaxis protein" Pprotein\_id\*"AAK78086.1" /product-"0-acetylhomoserine sulfhydrylase" /protein\_id="AAK78087.1" GIDSPYERPERPETTVETYRDTEEKCVDNIIEYLKQHKIL\* /organism="Clostridium acetobutylicum" /orgariam="ATCC 824" /db\_xref="ATCC:824" /db\_xref="taxon:1488" /product-"Adenylylsulfate kinase" /protein\_id="AAK78088.1" /db\_xref-\*GI:15022926\* /db\_xref-"GI:15022928" 2025. .3254 /gene="CAC0102" 2025. .3254 /gene="CAC0102" /gene="CAC0101" 271. 1665 /transl table=11 /codon\_start=1 /transl\_table=11 /codon\_start=1 /transl\_table=11 271. 1665 /gene="CAC0101" /gene="CAC0104" 3877. .5556 3877. .5556 /gene="CAC0104" EVLVERLNKLLKNE\* 3264. .3866 /gene-"CAC0103" /gene-"CAC0103" /codon start=1 /codon\_start=I /note="cysc" 3264 .3866 5556 1665 TOTIENAT. gene REFERENCE Sgo PEATURES CDS ä Ciceridam acetoburylicum ATCC824 section 11 of 356 of the ABC0722. ABC0722. Gills02225 1 (bases 1 to 1111)
1 (bas Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridlaceae; 959 GAATGCCCTTCACCCAAAGCAATGGCCAAGCAAGTTCTATGCTACCTTGAAGAAAGGGA 1018 688 CCTGACGGCGATTTCGTCGAGGTCTTCATGGACGTTCCTCTTCATGTGTGCGAGTCGAGA 747 902 GATGATCCATACGAACCACCAATTAATGGTGAGATAGTAATTA---AGATGAAAGATGA Gaps 422 GGGAAATCGACTAATATTTTATGGCACAATTGCTTGATTGGACAATCTGATAGACAGAAA 481 328 GAGAAAGCAGAAGAACATCGTGTGGCBCGAGATTCGATATGCAGATGCGACAGACAACAA 387 482 TIGCTGGGACAAAAAGGCTGTGTCGTATGGATAACAGGACTCAGTGGTTCAGGGAAAAGT 541 542 ACTUTIGCATGRIGACTIGAGTCGTGAGTTGCATTGCAGAGGCCACCTCACGTATGTACTT 601 GATGTGACAACCTCAGACATGGCCTAAATAGAGATTTAAGCTTTAAGGCAGAGAGCGT 661 508 GACGGCGACAATGTCCGTCACGGCCTTAACCGTGACCTCGCTTTCAAAGCAGGCACGC 567 562 GCAGAAATATACGAAGAGTIGGIGAAGIGGCAAAGCITTTIGCIGAIGCIGGIGGGIA 721 628 TGTATAGCAAGTITGATITCTCCGTACCGGAGACAGAGGCGCGTGCCTGGTTA 687 CCACATTCTAACTTTATTGAAGTATTTATTGATTTGCCCCTAAAAATTGTGAAGCTCGT 841 842 GATCCTAAAGGCCTATACAAGCTTGCACGTACAGGAAAGATTAAAGGTTTCACTGGAATT 901 3; Length 1311: Indels O; Mismatches 209; DB 8: Score 263.6; DB 8 Pred. No. 4.4e-52; Clostridium acetobutylicum 21.78; Conservative 1019 TATTICCAAGCTTA 1032 928 TATCTTGAGGGTA 941 Similarity Best Local Sim: Matches 402: Query Match DEFINITION ORGANISM MEDLINE 502 83 RESULT 8 AE007523 ACCESSION REFERENCE AUTHORS JOURNAL KEYWORDS PERSION TITLE ORIGIN

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ANBLI399 L GI:llss17
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Permatophyta; Wagnoliophyta; eudicoryledons; core eudicota;
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                                      DB 171710 CMGCGCCATCTGCCGCGATTTGGGCTTTTTCTGAGGCTGATCGTGAAAATATC 171651
                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui TAC
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Submitted (06-MAY-1998) Yasakkeu Wakemuta. Karusa DNA Research
Institute Department of Plant Gene Research; 1532-3, Yana,
Kasarau, Chiba 22-0812, Dapan (G-mall;ynakmutkazusa.oc.)P,
Tel. 84-136-22-395, Faxe 81-45-22,9934,
                                                                                                                                      614 CICAGACATGGCCTAAATAGAGATTTAAGCTTTAAGGCAGAAGACGGTGGAGAAATATA 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AATATTTTATGGCACAATTGCTTGATTGGACAATCTGATAGACAGAAATTGCTGGGACAA 493
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/note-"PS01223 Gamma-glutamyl phosphate reductase
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Pred. No. 5.7e-29;
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/protein_id="CAC92456.1"
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/gene="proB"
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Tristy 1940 Cedex, PRANKE /note="difference with the nucleotide sequence previously described; one more G at position 1332\* A Bacillus subtilis chromosome segment at the 100 degrees to 102 degrees position encoding 11 membrane proteins Macrology 144 (Pt 10), 3309-3312 (1997) Cloning and seguencing of 53 kbp from B. subtills chromosome Unpublished /organism-"Bacillus subtilis\* RPFASPANDQAGADACALFRISARLQLF" 1947. .2816 /codon\_start=1 /transl\_trable=11 /product='Yiry' /protein\_id="CAN70570\_1" /db\_xref="SPTRAHBL:006712" /db\_xref="SPTRAHBL:006712" /product-"Yirz" /protein\_id-"CAA70671.1" /db\_xref-"G1:2145365" /db\_xref-"SPTREMBL:006713" /product="SbcD" /protein\_id="CAA7069.1" /db\_xref="G1:2145363" /db\_xref="SPTREMBL:006711" /db\_xref-"taxon:1423" Location/Qualifiers 1, .53533 /transl\_table=11 /transl\_table=11 /note="putative" /note="putative" /transl\_table=11 QKRLLEARTSSSP" /codon\_start=1 /codon start=1 (bases 1 to 53533) (bases 1 to 53533) Seror, S. REFERENCE JOURNAL TOURNAL TOURNAL CDS CDS FEATURES CDS SOS TITLE TITLE COMMENT PFEYLYSKRPHGEDSRDMTVFKDDDGVAYLIYSSEVNSVLHIGFLTEDYLDYTPVMKR YWOGNREARALIFKHDIYTYNTSKTTOMFRALAMERSIANDRESIKGNESTGONK VPRLTTFFAGOTYVIELPGVYGARIFKANDRWIRADLROSRYWWLELVIGGPADOELEG Sequencing of regions downstream of addA (98 degrees) and citG (289 /translation-"MKKNNKYNKKSTSLHCNDAGGCRYSLLTIVWTVVGFFLVAHLIS LYSRKDNNIHQQVSSDQLQVVHHLAHPIVRELIRVEEEVLRMPPPRKRSPRTSKRRSR KPTPLVERFLDDKSPTRHLFFPGTKTAAFGPTKDMGNETSYYFPGKIWMDTOGNPTOA HGGGILLDVKSNTYVWYGEYKDGPTYHAHKKGPARVDIIGVGCYSSKDLWTWKNEGIV LGAEETNKTHDLHKSNVLERPKVIYNEKTEKYVWWHIDDANYTKASVGVAISNSPTG BCT 31-MAY-1997 complement(join(26074. .26457,26551. .26727,27046. .27117, dene; gene; gene; gener ytso gene; gene; 19128 ATTITITCAGGIAAAAGIAGICIGGCAIGIGCICITAGICGAGCITIGCACAAICGIGGA 19187 19188 AAGCTTTCGTATATACTTGATGATGATGGTTGACATGGTTTAAACAGCGATCTTAGT 19247 19308 GCAGATTCTGGTATTATCTGTATTGCAAGTTTAATATCTCCTTACCGGATAGAACGAGCT 19367 (bases 1 to 17287) defailing the nucleother. B. Vannier.F. and Seror.S.J. 17 kb nucleother. Sequence downstream of addAB of the Bacillus 584 CACCTCACGTATGTACTTGATGGTGACAACCTCAGACATGGGCTAAATAGAGATTTAAGC 643 703 GCTGATGCTGGTGTCATATGCATTGCTAGCTTGATATCTCCATACAGGAGGATCGTGAT 763 0; Gaps yisB c yith yith yith yisu nprB 644 TFTAAGGCAGAAGACCGFGCAGAAAATATACGAAGAGFFGGTGAAGFTGGCAAAGCTFTFF Medina, N., Vannier, F., Roche, B., Autret, S., Levine, A. and Roche, B., Autret, S., Levine, A., Vannier, F., Medina, N. and Seror, S.J. DB 8; Length 51860; yisG gene; yisM gene; yisT gene; yisZ gene; yitF gene; dene; dene; dene; gene; 76; Indels linear 19368 GCCTGCCGTGCATTATTACCACAAGSAGATTCATTGAGGTTTCT 19412 yisa Sacteria; Firmicutes; Bacillus/Clostridium group; 764 GCATGCCGTGCTCTACTTCCACATTCTAACTTTATTGAAGTATTT 908 degA gene; yirz gene; yisz gene; yisz gene; yirz gene; yitk gene; yitk gene; degrees) in Bacillus subtillis Microbiology 143 (Pt 10), 3305-3308 (1997) Score 163.4; DB B Pred. No. 7.2e-28; 3acillus/Staphylococcus group; Bacillus.
1 (bases 43091 to 53533) DNA B.subtills 54kb genomic DNA fragment. 0: Mismatches gene; gene; gene; gene; gene; dene: dene: dene; NFGFPSWSRVSIYWHSKWRLP" 53533 bp /db\_xref="GI:9757875" (bases 17288 to 43091) 13.4%; GI:2145361 subtilis chromosome Conservative Similarity Jupublished Medina, N., 109476.1 38015415 Seror, S. Duery how. Best Local Similar RESULT 11 BSY09476/c LOCUS 704 ACCESSION ORGANISM REFERENCE AUTHORS TOURNAL MEDLINE REFERENCE TOURNAL REFERENCE TITLE TITLE Q g g à g ô ò ò ò

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Bacillus/Staphylococcus group; Bacillus.

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Nature 390 (6657), 249-256 (1997) , Ogasawara, N., Yoshikawa, H. and Danchin, A. /note="similar to adenosylmethionine-8-amino-7-oxononanoate aminotransferase" /organism="Bacillus subtilis" /strain="168" /db\_xref-"taxon:1423" Location/Qualifiers /gene="yhxA" /function="unknown" (bases 1 to 210440) 1749. .2441 /gene="glpp" 1749. .2327 /gene="yhxA" 369. 1721 . . 210440

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FEATURES

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AUTHORS TITLE JOURNAL JOURNAL MEDLINE REFERENCE

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bb 170197 TCCCGGATGGGGAAAGTGCGGAAGTGTTTTGTTTTGTGAGGGGGCGAAACATTTAACGE 170138 Db 170137 CTTTATTTCTCCATTCCAGGAGGATGGATAGGTAGAGGGCTCTTTCCTAAAGGG 170078 732 GCTTGATATCTCCATACAGGAGGATCGTGATGCATGCCGTGCTCTACTTCCACATTCTA 791

10 others

ORIGIN   PACE   12.91, SCOTE 136.41, DB 8: Length 1146;		0 y 814 ANATTECRAROCTECTRACOCCUTACAGACTAT 883  D 714 GAMSTECTRACOAGACACTATACAGACTATACAGACACACAGACAGACAGAC	RESULTION  MANUSCATA
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FYDENHUMEETSGTRKKAAREGELPEGFMARK BASE COUNT 714 a 493 c 549 g 622 t ORIGIN Ouery Match 0 12.8%; Scored 155.6, no. 3: Length 2378; Best Local Similarity 60.1%; Pred. No. 2.6e-26; Matchee 279; Conservative 0; Mismatches 179; Indels 6; Gape

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GenCore version 5.1.3 Copyright (b) 1939 - 2002 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: November 1, 2002, 22:55:32 : Search time 234 Seconds (Valthout alignment) (Valthout alignment) (93:04:04:04:04:04:04:04:04:04:04:04:04:04:	11tle: US-09-720-384A-3 Perfect sore: 127	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 1736436 seqs, 858457221 residues	Total number of hits satisfying chosen parameters: 3472872	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match ON Maximum Match ON Maximum Match ION Maximum Maximum Sector ION Summeries	Database : N_Geneseq_032802:*	<ol> <li>/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*</li> <li>/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*</li> </ol>	3: /SIDS1/gcgdata/geneseq/genesegn-embl/NA1982.DAT:* 4: /SIDS1/gcgdata/geneseg/genesegn-embl/NA1983.DAT:*	5: //SIDSI/gogdata/geneseq/jeneseqn-embl/NA1984 DNT:* 6: //SIDSI/gogdata/geneseq/geneseqn-embl/NA1985.DNT:*		12: /SIDS/1904 but Jennesey/senseary-min. Mxi 30: 1.Att; - 13: /SIDS/1904 but Jennesey/senseary-min. Mxi 30: 1.Att; - 14: /SIDS/1904 but Jennesey/senseary-min. Mxi 30: 1.Att; - 14: /SIDS/1909 but A/genesey/senseary-min. Mxi 30: 1.Att; -	16: /SIDSI/geddata/geneset/genesett-emini/Nal.99.DAT:* 16: /SIDSI/geddata/geneset/genesett-emini/Nal.99.DAT:* 17: /CTRCI /ordata/ceneset/genesett-emini/Nal.99.DAT:*	18: /SIDSI/gcdata/geneseq-geneseq-embl/NA197.Drr.* 19: /SIDSI/gcdata/geneseq-geneseq-embl/NA197.Drr.* 19: /SIDSI/gcdata/geneseq-geneseq-ampl/NA199.Drr.*	20: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1999.Dar.*	22: /SIDSI/gcgdata/genescy/genescqq=mbi/NA2001a.bAT:* 23: /SIDSI/gcgdata/genescy/genescq=mbi/NA2001a.bAT:*	24: /SIDSI/gcgdxta/geneseq/geneseqn-embl/NA2002.DNT:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.		Result Query No. Score March Length DR ID Description	2207 100.0 1217 21 AA250160	359.6 29.5 928 21 AAZ50163 339.8 29.5 928 21 AAZ50163	320.4 26.3 627 21 AAZ3UL62	5 256.4 24.4 1068 21 AAZ32456 AZBIGGESS TABLIA 7 256.4 24.4 1108 21 AAZ32466 AZBIGGESS TABLIA	296.4 24.4 1183 21 AAC45659 290 23.8 1130 21 AAC49070

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Adenyiyisuiphate kinase; Adenosine-5'phosphosuiphate kinase; ABS kinase; 3'-phosphosuiphate, PABS' sulphate assimilation; 3'-phospho-adenosimilation; wheet; clone wil.pkilii.e2; transgenic plant; screen; antibody; 8s.
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Falco SC.
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                                                                                               .084 GGACACAATAAGATCTGTTGTTGGTCACATGAATA--AAGGCATCAACATGTAGGAAGT
                                                                                                                                                                                                                                                                                     t- "Soybean APS kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present expenses is a comb encoding when deeplylluphtar kinese (MSS kinese), also known as adenoating-5; phesphosauphane kinese. This is obsidented from the companion of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 TTCACCCAAAGCAATGGCCAAGCAAGTTCTATGCTACCTTGAAGAAAACGGATATTTGCA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       populides are useful for producing antibodies, that are used to screen and isolate cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 GCCCGGGGAGGCCCCGCACAGCCCAGTGAAGGAGAAGCCTGTAATGTCGAACATTGGGAA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 GCCCTCAATGSATCACCCAATGCAGGTATCGACCTCTGTGACCTCTAACTCTTGCGAA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 GGGACAAAAAGGCTGTGTCGTATGGATAACAGGACTCAGTGGTTCAGGGAAAAGTACTCT 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 289; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 928 BP; 285 A; 168 C; 250 G; 225 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le-80;
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65.5%; Pred. No. 1.1
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Anderson St.
                                                                                                                                                                                                                                                                                                                                     assimilation protein in plants
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Allen SM.
                                                                                      WPI; 2000-182430/16.
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Salco SC.
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990S-013945
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25 - FRB 1999

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14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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08-JUN-1999;
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                                                                                                                                                                                                                                                                                                          373 GATAGACAGCAGCTCAGCAACAAGGCTGTTATATGGCTAACTGGCCTCAGCGGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                          590 ACCTATGTACTTGATGGTGACAACCTCAGACATGGCCTAAATAGAGATTTAAGCTTTAAG 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553 GCAGAAGATCGTTCTGAAAACATTAGAAGGATTGGTGAGGTGGCAAAACTCTTTGCAGAT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673 AGAGCACTACTTTCAAAAAGGAGATTTTATTATTCATAGATGTTCCACTACATAGTGTG 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 ATGTCGAACATTGGGAAATCGACTAATATTTTATGGCACAATTGCTTGATTGGACAATCT 469
                                                                                                                                                                                                                                                                              470 GATAGACAGAAATTGCTGGGACAAAAAGGCTGTGTCGTATGGATAACAGGACTCAGTGGT 529
                                                                                                                                                                                                                                                                                                                                                                                              TCAGGGAAAAGTACTCTTGCATGTGCACTGAGTCGTGCATTGCATTGCAGAGGCCACCTC 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 TCTTACATCCTTGATGGTGACAATATTCGGCATGGTCTAAACCAGGATCTTAGTTTTAGA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650 GCAGAAGACCGTGCAGAAAATATACGAAGAGTTGGTGAAGTGGCAAAGCTTTTTGCTGAT 709
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                                                                                                                Gabs
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                                                        Score 338.8; DB 21; Length 936;
Pred. No. 1.9e-75;
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                                                                                                          0; Mismatches 177: Indels
Sequence 936 BP; 266 A; 206 C; 240 G; 224 T; 0 other;
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                                                        Ouery Match 27.8%;
Best Local Similarity 71.5%;
Matches 445; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenylylaulphate kinase; Adenosine-5'phosphosulphate kinase; APS kinase; Prospho-adenosine-5'phosphosulphate; PRPS; sulphate sas-finilation; corn; clone eenin, kNOOBS-IDG, transgente plant; sereen; antibody; ss.
                                                481 TICACAGGAATAGATGATCCGTATGAGTCTCCCTTGAACTGTGAGATAGAGTTGAAAGAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 AGCAGCGCCCGGGGAGGCCCCGCACAGCCCAGTGAAGGAGAAGCCTGTAATGTCGAACAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule and chimeric gene encoding an adenosine-5' phosphosulfate kinase, useful for altering expression of sulfate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Corn APS kinase-1"
/note= "Derived from clone cen3n.pk0088.b10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corn Adenylylsulphate kinase-1 cDNA clone.
                                                                                                                                                             1010 GAAAACGGATATTTGCAAGCTTAGTA 1035
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                                                                                                                                                                                                             601 GACAAAGGTTTCCTTCAAAACGAGTA 626
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842 GACGTGAAGGAGGAACTTCTCCTATCGAAATGGCGGAAAAGGTCGTCGGATACTTAGATA 901
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                                                                                                                                              Arabidopsis thallana DNA fragment SEQ ID NO: 14353
                             1011 AAAACGGATATTTGCAAGCTTAGTATGTAT 1042
                                      902 ACAAGGTTATCTTCAAGCATAACATACTTCT 933
                                                                                           AAC36588 standard; DNA; 1175 BP
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28-MAY-1999;
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pred. No. 9.7e-65;
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GCGAGGCGAGGCATCAAAGGCTCTTTACAAGCTTGCTCGTGCTGCAGGAAAGATCAAAGGTT 787 

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		99 591 CGTMTGTMCTRGATGGTGACAMCCTCAGACATGGCCTAAATAGAGATTTAAGCTTTAAGG 650  DD 479 GTMTATTGTTAAGGTGATAATGTTAAGGCTGATAAACGTGATGGTTAAACGTGATTAAACGTAATGTTAAAGGTAATGTTAAAAGGTAATGGTAAAATGTAAGGATAAGGTAAATGGTAAAATGTAAAAATGGAAAAAA	0y         651 CABANGACCITGCAGAJAANANACABAGACITGCAGAACTATTTCCTGAYG         710           bb         513 CYAGGAACCGAGAAANANTCCTAGARAGCTTGTAGACTTTTTTCCGGAG         598	CTGGTGTCATATGCATTGCTTGATATCTCCATACAGAAGATCGTGATGCATGC		Oy 831 GTGAAGCTGGTGAVCCTAAAGGCTATACAAGCTGCAACAGCATAAAGGTTAAAGGTT 890  Db 719 GCGAAGCGGGGGGGGGGTCTTACAAGCTTGCTGGTGAAAAGTTAAAGGTT 778  D1 3 GCGAAGGGGGGGGGGGGGGGGTTTACAAGCTTGCTGGTGGGGAAAAACAATAAAGGTT 778	69         891         ПОСТОВОВАТОВАТОВЛЕСЬИЯ ОСТАВЛЕНИЯ         950           Db         779         ТРАСОВОВАТОВИТОВОТНОСТВИВОВОЕННОЕМИТОВОВИТОВОВИВЕННОЕМИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИИ В 100 МИНИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВНОЕМИ В 100 МИНИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВИТОВОВНОЕМИ В 100 MINITORUS В 100 M	Qу         951 АЛФИТОВАВАЛТОССТВИВСЕДАТОВОСТВАТИТОСТВОВАВ           Db         833 ФОСОСТВАТОВОТОВОТОВ В В В В В В В В В В В В В В	0y 1011 AAAGORANTIGOAAGCTAAGAKAYATA 1042 Db 893 ACAAGGTAACTTCAAGAKAACATACTTC 934	RESULT 8 NA Act45659 standard: DNA: 1183 BP.	AC AAC45659; DT 18-0CT-2000 (first entry)	AAA DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47294. xx	KM Hybridisation assay; genetic mapping; gene expression control; KM protein identification; signal transduction perhaps; KW metabolic pathesy; promoter; termination sequence; ss.		XX XX PD 06-SEP-2000.	XX PF 25-PEB-2000; 2000EP-0301439.	25-FEB-1999; 05-MAR-1999; 09-MAR-1999;	PR 23-WRF 1995; 9018-0215788 PR 25-WRF 1995; 9018-02156-064 PR 29-WRF 1995; 9018-0216784.	06-APR-1999; 08-APR-1999; 16-APR-1999;

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TCGACTAATATTTTATGGCACAATTGCTTGATTGGACAATCTG 470 TCGACAAATATAAAGTGGCATGAATGTTCTGTTGAGAAAGTTG 368 GGACAAAAAGGCTGTGTGGTATGGATAACAGGACTCAGTGGTT 530 GATCAGAAAGGATGTGTGATTTGGGTCACGGTCTTAGTGGTT 428 GCATGTGCACTGAGTCGTGAGTTGCATTGCAGAGGCCACCTCA 590 CCTTGTGCTTTGAATCAGATGTTGTATCAAAAGGGGAAGCTTT 488 GACAACCICAGACAIGGCCIAAAIAGAGAIIIAAGCIIIAAGG 650 GATAATGTTAGGCATGGCTTAAACCGTGATCTTAGCTTTAAAG 548 AATATACGAAGAGTTGGTGAAGTGGCAAAGCTTTTTGCTGATG 710 AATATTCGTAGAGTTGGAGAGGTTGCTAAGCTTTTTGGGGATG 608 GCGACTTTGATATCTCCTTATAGAACAGATAGGGACGCTTGTC 668 ICTAACTITATIGAAGTATITATIGATITIGCCCCTAAAATIT 830 GGAGATTTGTTGAGGTGTTCATGGATGTACCGCTTAGTGTTT 728 AAAGGCCTATACAAGCTTGCACGTACAGGAAAGATTAAAGGTT 890 CCATACGAACCACCAATTAATGGTGAGATAGTAATTAAGATGA 950 CCTTACGAGCCACCATTGAACTGCGAG-----ATTTCTCTAG 842 TCTCCTATCGAAATGGCGGAAAAGGTCGTCGGATACTTAGATA 902

4.4%; Score 296.4; DB 21; Length 1183; 8.0%; Pred. No. 1e-64; ve 0; Mismatches 196; Indels 6;

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                   GIACTIGAIGGIGACAACCICAGACAIGGCIAAAIAGAGAIIIAAGCIIIAAGGCAGAA 655
                                519 ATACTTGATGGTGACATGTTCGACATGGTTTAAACAGCGATCTTAGTTTGGAAGCAGT 578
                                                                                                                                                                                776 CTRCTTCCACATTCTAACTTTAATGAAGTATTATTGATTTGCCCTAAAATTTGTGAA 835
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                                                                                                                                                                                                                                                                                                                                                GGAATTGATGATCCATACGAACCACCAATTAATGGTGAGATAGTAATTAAGATGAAAGAT 955
                                                                                 656 GACCGTGCAGAAATATACGAAGAGTTGGTGAAGTGGCAAAGCTTTTTGCTGATGCTGGT
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Matches 389; Conservative
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13-0CT-15
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The limenting relates to solution of could sequence and/or release the first collection of collectio
                                                                                                                                                                                                                                                                                                                                          solation of polynucleic acids useful for producing transgenic plant by solating genes involved in tolerance to environmental stress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 ACCGAAACATAGAACAATTGGTGAGGTGAGGTAGTTGTTTGCTGAGGTCGGAGTCATT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653 CCTGACGCCGATTTCGTCGAGGTCTTCATGGACGTTCCTCTTCATGTGCGAGTCGAGA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422 GGGAAATCGACTAATATTTTATGGCACAATTGCTTGATTGGACAATCTGATAGACAGAAA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 ITGCTGGGACAAAAAGGCTGTGTGGTATGGATAACAGGACTCAGTGGTTCAGGGAAAAGT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 ACTCTIGGATGIGGACTGAGTCGTGAGTIGCAITTGCAGAGGCCACCTCACGTATGTACTT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562 GCAGAAAATATACGAAGAGTTGGTGAAGTGGCAAAGCTTTTTGCTGATGCTGGTGTCATA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACATICTAACTITATIGAAGTATITATIGATITGCCCCTAAAATITGTGAAGCTCGT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGATCCATACGAACCACCAATTAATGGTGAGATAGTAATTA---AGATGAAAGATGAG 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 GATCCTAAAGGCCTATACAAGCTTGCACGTACAGGAAAGATTAAAGGTTTCACTGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602 GAIGGIGACAACCICAGACAIGGCCIAAAIAGAATIIAAGCITIIAAGGCAGAAGACCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.7%; Score 263.6; DB 21; Length 917; 65,5%; Pred. No. 1.7e-56; tive 0; Mismatches 209; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 917 BP; 244 A; 220 C; 229 G; 224 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 218-220; 312pp; English
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Matches 402; Conservative
                                                                                                                                                                                                                                   Verbruggen N;
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                     40200008187-A2
                                                                                                                                                 34-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTACTTGATGGTGACAAACCTCAGACATGGCCTAAATAGAGATTTAAGGTTTAAGGCAGAA 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         776 CTACTTCCACATTCTAACTTTATTGAAGTATTTATTGATTTGCCCCTAAAAATTTGTGAA 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 699 TRATTACCACACACACACTTTCATTCACTCATTCACTCCACTCCACTCCACTCCACTCCACTCTTTCTCAA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         836 GCTCGTGATCCTAAAGGCCTATACAAGCTTGCACGTACAGGAAAGATTAAAGGTTTCACT 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              896 GGAATTGATGATCCATACGAACCACCAATTAATGGTGAGATAGTAATTAAGATGAAAGAT 955
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                                                                                                                                                                                                                                                                                                                                                                                         416 AACATTGGGAAATCGACTAATATTTATGGCACAATTGCTTGATTGGACAATCTGATAGA 475
                                                                                                                                                                                                                                                                                                                                                                                                                   339 ATCARIGGAAAGCAAAAGAACAIIGTVIGGCAIGAIIGICCCGIIACIAAAICCGACAGG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAAATTGCTGGGACAAAAGGCTGTGTGTATGGATAACAGGACTCAGTGGTTCAGGG 535
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                          0; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                   Score 288.4; DB
Pred, No. 1e-62;
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                                                                                                       990S-0161406.
99US-0161359.
99US-0161360.
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99US-0161992
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   773 GACGACCCTTACGAGGCACCAGTGAATTGCGAGGTAGTGCTGAAACACACAGGAGGAGGCAC 832
                                   Hybridisation assay; genetic mapping; gene expression control; protein identification, signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                Arabidopsis thaliana DNA fraqment SEQ ID NO: 35008.
                      AAC42294 standard; DNA; 948 BP
                                                        25-FEB-2000; 2000EP-0301439
                             17-0CT-2000 (first entry)
          1019 TATTTGCAAGCTTA 1032
            893 TATCTTGAGGCCTA 906
                                           Arabidopsis thaliana
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us-09-720-384a-3.rng

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	3; 3; 1GACAGAI
	Length Indels VTCTGATA
	DB 21; Length 948 :56; 209; Indels 3: "GGACAATCTGATAGACAC
	29-077-1599, 9980-0513142, Sorre 265.6; um 21; Length 948; sept. Choisto, 20, 174; Sorre 265.6; um 21; Length 948; sept. Choisto, 21,174; Sorre 265.9; pred. 21,74; Sorre 265.9; pred. 27,95; pred. 3; caps Mechas 402; conservative 0; Klamachas 209; indem 3; caps Mechas 402; conservative 0; Klamachas 209; indem 3; caps Mechas 402; conservative 0; Klamachas 209; indem 3; caps Mechas 403; conservative 0; Klamachas 209; indem 3; caps Mechas 200; conservative 0; Klamachas 209; indem 3; caps Mechas 200; conservative 0; Klamachas 209; indem 3; caps Mechas 200; conservative 0; Klamachas 200;
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	r-1999; 99US-0162) cch al Similarity 65: 402; Conservative SGGAATCGACTAATTTT
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Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
protein bathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 225; DB 21; Length 714;
Pred. No. 8e-47;
0; Mismatches 190; Indels 87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 ATGTCGAACATTGGGAAATCGACTAATATTTATGGCACAATTGCTTGATTGGACAATCT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGTCGACAGTGGGAAATTCAACGAACATATTTTGGCAAGAATCCCCCATTGGGAAAACT 60
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14-0CT-1999;
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900 014141 Query Match
Best Local Similarity 65.8%;
Matches 318; Conservative 0 ò a

Score 198.2; DB 21; Length 483; Pred. No. 3.8e-40; 0; Mismatches 138; Indels 27; Gaps

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Claim 3; Page 32; 42pp; English.
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         209
                                                                                                                          14 GCAGAGGATAGAGTGGAAAATATACGCAGGGTCGGAGAAGTAGCCAAACTCTTTGCGGAT 300
                                                                                                                                                        GCTGGTTAATCTGTATTGCCAGCCTCATATCCCCGTATAGAAAAGACCGTGACGCCTGC 360
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                                                                            590 ACCIATGRACTIGATGGTGACAACCTCAGACAIGGCCTAAATAGAGATTTAAGCTTTAAG 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule and chimeric gene encoding an adenosine-5' phosphosulate kinase, useful for altering expression of sulfate essamilation protein in plants
                                                                                                                   GCAGAAGACCGTGCAGAAATATACGAAGAGTTGGTGAAGTGGCAAAGCTTTTTGCTGAT
                                                                                                                                                                                             /product= "Rice APS kinase"
/note= "Derived from clone rl0n.pkl12.oll"
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## Sequence 431 BP: 126 A: 78 C: 112 G: 112 T: 3 other:

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                                                 0; Gaps
                                                                                                   424 GARATCGACTARTATTTTATGGCACARTTGCTTGATTGGACARTCTGATAGACAGAAATT 483
                                                                                                                                 66 GAAGGCGTCCAATATCTTCTGGCATGATTCTGCAGTTGGCCAGCTGATCGGCAGAAGCT 125
                                                                                                                                                                                                      484 GCTGGGACAAAAAGGCTGTGTGTATGGATAACAGGACTCAGTGGTTCAGGGAAAAGTAC 543
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    DB 21, Length 431;
                                                 94; Indels
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72.9%; Pred. No. 6.5e-40;
dve 0; Mismatches 94;
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Search completed: November 1, 2002, 23:43:31 Job time : 239 secs



202, App 202, App 21, Appl 4, Appli 1, Appli 40, Appli 136, Appl

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Hangan, Jorgen
Johannesen, Fita Francke
Pederasen, Nogens Bobhl
Sorensen, Steen Bech
INVERTION: Welchod of producing a composite
Fremented beverage using genetically modified yeast
                                      sequence 1 Sequence 2 Sequence 2 Sequence 1 Sequence 2 Sequence 4 Sequence 4 Sequence 4 Sequence 4 Sequence 4 Sequence 6 
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TIP 7.3007.2
US 90 0.013 868.A.1
US 90 007 005.17
US 90 005.1
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TELECOMMINICATION INFORMATION:
TELEPHONE: 202-672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11near
MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-153-310-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-Sep-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 41, Application US/09153310
Patent No. 6326191
GENERAL INFORMATION:
APPLICANT: Gjermansen, Claes
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INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1160 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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5640.301 Million cell updates/Sec
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- GPIS_APPRODERAZ/Ina/SA_COMB.Seq.*

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- GPIS_APPRODERAZ/Ina/SA_COMB.Seq.*

- GPIS_APPRODERAZ/Ina/AB_COMB.Seq.*

- GPIS_APPRODERAZ/Ina/AB_COMB.Seq.*

- GPIS_APPRODERAZ/Ina/AB_COMB.Seq.*

- GPIS_APPRODERAZ/Ina/AB_COMB.Seq.*

- GPIS_APPRODERAZ/Ina/ABASKTISB.Seq.*
                                             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-113-452-412

US-09-104-669-11

US-09-105-764-11

US-09-165-764-11

US-09-165-764-11

US-09-165-744-14

US-09-165-749-12

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US-08-125-468-1
US-08-174-933-1
US-09-165-264-13
US-08-977-0011-2
US-09-162-0218-1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                             660 TCGTGTGTGTGTGTGTGTTGTTTCCCGATACAGAGACAGAGACAGAGCC 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        770 CGTGCTCTACTT-----CCACATTCTAACTTTATGAAGTATTTATTGATTTGCCCCTA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      824 AAAATTTGTGAAGGTCGTGATGCTAAAGGCCTATACAAGGTTGCACGTACAGGAAAGATT 883
DB 4; Length 1160;
12.9%; Score 156.4; DB 4; Length 1
ilarity 60.4%; Pred. No. 4.6e-31;
Conservative 0; Mismatches 176; Indels
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SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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FILING DATE: Herewith
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Patent No. 5817482
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3174 Porter Drive
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IBM Compatible
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ADDRESSEE: Incyte Pha
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
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                                  Best Local Similarity
Matches 278; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 AGACATGGCCTAAATAGAGATTTAAGCCTTTAAGGCAGAAGACCGTGCAGAAAATATACGA 676
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Pred. No. 2e-26;
0; Mismatches 185; Indels
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APPLICANT DOMENT. F.
APPLICANT SCHEEKINGER, F.
APPLICANT FALKER, F. G.
APPLICAN
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1800 Diagonal Road, Suite 500
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COMPUTER READABLE FORM:
COMPUTER: ISM PC compatible
computer: ISM PC compatible
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Patent No. 5670367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 2506 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catches 266: Conservative
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LIBRARY: LUNGN
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APPLICANT: Buchholt, H.
TITLE OF INVENTION: PROCESS FOR STABILIZING PROTEINS IN AN
TITLE OF INVENTION: PROCESS FOR STABILIZING PROTEINS IN AN
FILE REPERENCE: DYOLA, 001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.7%; Score 45.6; DB 4; Length 1323; 
Best Local Similarity 52.7%; Fred, No. 0.017; 
Matches 99; Conservative 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 3.7%; Score 45.6; DB 3; Length 1323; I Similarity 5.7%; Pred, No. 0.077; O. 19; Conservative 0; Mismatches 89; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/6-06
EXRAIDER PELLNA DENE: 1999-6-06
EXRAIDER PELLNA DAME: 1999-6-55-18
EXRLIER PELLNA NUMBER: PCT/EP96/03051
EXRLIER PELLNA DAME: 1996-07-12
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; ORGANISM: Citrus sinensis var. Navel
US-09-413-452-3
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Patent No. 6268195
GENERAL INFORMATION:
APPLICANT: Christensen, T.
APPLICANT: Thorsoe, H.
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Best Local Similarity
Matches 99; Conserve
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us-09-720-384a-3.rni
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3.94; Score 47.8; DB 1; Length 7218;
Best Local Similarity 4.0%; Pred: No. 10097;
Matches 16; Conservative 217; Mainaches 164; Indels 0;
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                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,768
REPERRACE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
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PILITION ON SEA SANG-1991
NAME: AGNET SEEPHEN SEE
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09413452
Patent No. 6083540
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
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                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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APPLICANT: Christensen, T.
APPLICANT: Thorsoe, H.
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kreiberg, J. APPLICANT: Buchholt, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-232-463-14
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FILE REFERENCE: 44747

TYPE: DNA

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GENERAL INFORMATION: APPLICANT: Vinayage

US-09-165-264-12/c

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APPICANT: Spekier, Priscilla A. TILLICANT: Web Lily TILLOR THEORY WEB LILY TITLE OF THEORYTON: Compositions and Methods for Treatment of Herpeavirus TITLE OF THEORYTON: Compositions and Methods for Treatment of Herpeavirus
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STEET: One Liberty Place, 46th floot
CITY: Philadelphia
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                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.6%; Score 43.4; DB 2; Best Local Similarity 51.3%; Pred. No. 0.082; Matches 98; Conservative 1; Mismatches 92;
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                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
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FILING DATE: 02-JUNE-1995
CLASSIFICATION: 435
                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WOOGCOCK,
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                       PILING DATE:
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45 ACACGCAGCAACCACCGAGCCCAGCGCCCGGCCCAGCCAGGGCCAACGGCAAGGCA 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . CTHER INFORMATION: Description of Artificial Sequence:Primer sequence
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APPLICAT: TREADY, MALICA
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APPLICAT: TREADY, MALICA
TITLE OF INVESTIGATION OF STREET
TITLE OF INVESTIGATION OF STREET
WHINER OF SEQUENCES: 12 COLING TIES
WHINER OF SEQUENCES: 12 COLING TIES
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TITLE OF INVENTION: Multi-Loci Genomic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09165264
Patent No. 6197510
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Patent No. 5965397
GENERAL INFORMATION:
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APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
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APPLICATION NUMBER: US 08/065,146

Cambridge

RESULT 7 US-09-014-969-14

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150 ATCCACAGGGGGCCCCCGGCCCCCCGGGCTCCCCTAGGGATGCGCCCCGG 209
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APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 ATCCATGGCCTCACTCCCCGTTCCTCACACTCTTCCGCGGGTCTCGCC 265
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233 South Wacker Drive/6300 Sears Tower
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Esquence II. Application US/09165264
GENERAL NEOSATION. INCOMENTAL NEOSATION.
TITLE OF PREMERONE. Multi-loci Genomic Analysis
FILE REPREMERS. 4447
CURRENT PARLICATION WHORES: US/09/05,264
OURRENT FILMS DAYE: 1999-10-01
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; Sequence 87, Application US/08474379C
; Patent No. 5977305
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COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
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SEQ ID NO 14
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3.54; Score 42.8; DB 1; Length 12001;
Best Local Similarity 51.64; Pred. No. 0.24;
Watches 98; Conservative 0; Manatches 92; Indels 0;
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replic
                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REPREME/DOCKET NUMBER: DFCL-0029
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; Sequence 11, Application US/09165264
; Patent No. 6197510
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TELEPOHNUR: (12) 568-100
TELEPOHN FOR SED. DN: 11:
SEQUINCE CHARACTERISTICS:
TENENT: 12001 Dass pairs
TYPE: nucleic acid
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                          CLASSIFICATION:
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6300 Sears Tower, 233 South Wacker Drive
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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USCATION: join(743..1648, 1651..2661)
US-07-688-352C-21
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                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20 APR-1990
ATTORNEY AGENT INFORMATION:
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ZIP: 60606-600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25447
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TELEX: 25-3856
INFORMATION POR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 3131 base pairs
                                                                                                                                                                                                                                                 FILING DATE: 20-07 PRINCE DATE: 20-08 OF THING DATE: 20-08 OF THING ATTORNEY AGENT INFORMATION: NAME: 2544 REGISTRATION NUMBER: 2544
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FILING DATE: 19910419
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STREET: 630v.
CITY: Chicago
TOR: Illinois
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MOLECULE TYPE: CDNA
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 3.5%; Score 42.4; DB 2; Length 1481; all Similarity 64.0%; Pred. No. 0.12; 64; Conservative 0; Mismatches 36; Indels 0;
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ADDRESSEE: Bicknell
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             SOPTHARE: Patentin Release 41.0, Version 41.30
SOPTHARE: Patentin Release 41.0, Version 41.30
APPLICATION NUMBER: US/06/474,379C
CLASSIFICATION: 435
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PRODE APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
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FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/07/688,352C
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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LOCATION: 1..1
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0: Gaps

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OTHER INFORMATION: /note= "Nucleotides 429-427 and 634-670 may OTHER INFORMATION: represent Infroms, sequence may have frame shifts at OTHER INFORMATION: nucleotides 328, 592, 1590 and 1592.*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%, Score 42.4; DB 3; Length 3131; Beast Local Smilarity 64.0%; Fred No. 0.16; Masatches 64; Conservative 0; Masatches 36; Indels 0.
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APPLICANT: Colleelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
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ADDRESSE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSE: Bicknell
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STREET: Street
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US-08-206-1888-21
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FILING DATE: 19910419
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APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGBNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application PC/TUS9102714 GENERAL INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (312) 346-5750
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INFORMATION FOR SEQ ID NO: 20
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 3131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                              NAME/KEY: misc feature
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MEDIUM TYPE: Floppy
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STATE: Illinois
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CLASSIFICATION:
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                                                                                                                                   TOPOLOGY:
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OTHER INFORMATION: may represent introduce may have frame shifts at nucl
OTHER INFORMATION: 592, 1590 and 1592,"
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64.0%; Pred, No. 0.16;
tive 0; Mismatches 36; Indels 0; Gaps
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APPLICANT. Objectil, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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REIDIN TIER FORM (15K
COMPOTER: INFO COMPATIBLE
COMPOTER: INFO COMPATIBLE
SOFTER: PCOMPATIRE (15K)
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STATE: Illinois
COUNTR: United States of America
ZIP: 6066-6402
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FILING DATE: 01-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/08206188B Patent No. 6100025 GENERAL INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36.107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36107
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TELEPHONE: 312/474-6300
                                                                                                                            TELERAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
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nucleic acid
EDNESS: Single
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Best Local Similarity 64.0%
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
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CLASSIFICATION:
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Title:	US-09-720-384A-3
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27472414 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: Searched:

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		Description	BE357876 DG1 22 A0	BE355111 DG1 113 B	BE361884 DG1_82_H0	AW922946 DG1_47_E0	BE361874 DGI_82_G0	BF484142 WHE1788_G	AW052991 614077E08	BG873962 MEST44-F0	AW560397 EST315445	BI427055 saq10q11.			BG126657 EST472303	BI320536 sah56h02.	AW056154 660004H03	AW288601 618069F05	BII78754 EST519699
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SUMMARIES		ΩI	BE357876	BE355111	BE361884	AW922946	BE361874	BF484142	AW052991	BG873962	AW560397	BI427055	BM407099	BF631366	BG126657	BI320536	AW056154	AW288601	BI178754
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	œ	Query	48.5	47.9	34.7	33.6	32.9	28.3	27.2	26.2	25.0	24.7	23.4	22.7	22.6	22.3	22.0	21.8	21.5
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An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
Contact. Cordonnier-Pratt MM
Department of Botany
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Clones to be sequenced were prepared by mass excision."
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Pred. No. 1.6e-76;
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Best Local Similarity 93.6%;
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(History was Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum. Cordonnier-Pratt, M. M., Gingle, A., Marsala, C., Sudman, M. and Pratt Page AW922946 19-JUL-20 T21 bp mRNA linear EST 19-JUL-20 DG1 47\_E04.gl\_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA 1084 GGACACAATAAGATCTGTTGGTCACATGAATAAAAGGCATCACATGTAGGAAGTAA 1143 964 CCCTTCACCCAAAGCAATGGCCAAGCAAGTTCTATGCTACCTTGAAGAAAACGGATATTT 1023 301 CCTTCCCCAAAGCAAGTTCTATCATACATAGAAGAAGGAAATTT 360 418 GGACACAATATGATCTGTTG-----GCCATGAATAAAAGGCATCAACACATAGCAAGTAA 472 Gaps 737 ATATCTCCATACAGGAGAGATCGTGATGCATGCCGTGCTCTACTTCCACATTCTAACTTT 796 GA 30602-7271, USA 8; 33.64; Score 409.2; DB 9; Length 721; Larity 90.14; Pred. No. 2.5e-50; Conservative 0; Mismatches 43; Indels 8: ain "Est destabase from Sorghum: dark-grown seedlings Inpublished (2000) Cootnest, Todoniag-Part MM Pepartment of Bother Part MM The University of Geograph, 2002, Athens, 04 30602 Plant Sciences Building, Rm. 2502, Athens, 04 30602 473 CAGAGGGGCAGTTGTTCAGAAGGGAATACAGATTCATTCGTTCA 519 High quality sequence start: 23 High quality sequence stop: 703 POLYA-No. AW922946 AW922946.1 GI:8088771 Seq primer: PolyTMix (bases 1 to 721) Tel: 706 542 1860 Fax: 706 542 1805 Sorghum bicolor Local Similarity sorghum. is 20. 463; Query Match source Best Loca Matches SOURCE BASE COUNT TITLE ACCESSION REFERENCE AUTHORS RESULT 4 AW922946 KEYWORDS PEATURES us-09-720-384a-3.rst VERSION COMMENT ORIGIN SDOOR ò g ò ò 6 ò g ó q ò £ BE351884 110-2012 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA Organizate Storpham bitolor\*
(Alizaret-tutoni.68)
( Sorghum bicolor Sorghum bicolor Rearyolar Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyra; Agnollophyta: Liliopsida; Poales; Poaceae; PACC Teder Paricoloflese, Addropogoneae; Sorghum. Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt 664 AGAAAATATACGAAGAGTIGGIGAAGIGGCAAAGCITITIGCIGAIGCIGGIGICAIAIG 723 CATHGOLDGCTTGATATCTCCATACAGAGAGAGATGGTGATGCGTGCCGTGCTGCTTGCCTTCC 783 84 ACATTCTAACTTTATTGAAGTATTTATTGATTTGCCCCTAAAAATTTGTGAAGCTCGTGA 843 AGAȚICTAACTȚIATICAAGTAȚITATGGATȚIGCCCCTAAAAATTGTGTGAAGCTCGTGA 180 844 TCCTAAAGGCCTATACAAGCTTGCACGTACAGGAAAGATTAAAGGTTTCACTGGAATTGA 903 181 TCCTAAAGGTCTGTACAAGCTTGCACGCACAGGAAAGATTAAAGGTTTCACTGGAATTGA 240 904 TGATCCATACGAACCACCAATTAATGGTGAGATAGTAATTAAGATGAAGATGAGGAATG 963 ---CCCATGATAAAAGGCATGAACAC 1 AGAAAATATACGAAGAGTTGTGTGAAGTGGCAAAGCTTTTTGCCGATGCTGTATCATATG 60 Gaps USA impublished (2000)
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The Un 8 Query Match 34.7%; Score 422.2; DB 10; Length 746; Sest Local Similarity 90.34; Pred. No. 3.2e-52; Score 424; Matches 475; Conservative 0; Mismatches 43; Indels B; Motches 476; Conservative 0; Mismatches 43; Indels B; J.H. An EST database from Sorghum: dark-grown seedlings High quality sequence start: 30 High quality sequence stop: 719 598 CCATTACTTGTGGACACAATATGATCTGTTG-1133 GTAGGAAGTAACAGAAGGTACGGTT 1157 Location/Qualifiers 653 ATAGCAAGTAACAGAGGCGCAGTTT 677 Email: mmpratt@uga.edu BE361884.1 GI:9303441 Sed primer: PolvTM1x ø sequence RE361884 sorghum. is 20. Source DEPINITION BASE COUNT ORGANISM TITLE JOURNAL COMMENT 724 19 ACCESSTON BE361884 REPERENCE RESILT 3 KEYWORDS PEATURES VERSION SOURCE ORIGIN ŏ 2 à g ò 용 ó ð

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BASE COUNT 199 a 121 c 184 g 225 t ORIGIN	Ouery Match Best Load Statistity 32.34; Score 400.2; DB 10; Length 699; Best Load Statistity 69.39; Pred No. 5.1e-40; Indets 8; Gaps 2; Matches 43; Conservative 0; Missatches 43; Indets 8; Gaps 2;	Oy 686 GAMCTGCCAAACTTTTTGCTGATGCTCATATGCTAATCTAACTTAATTGCTAACTTATTTTTTTT	0y 746 TACAGAGAGARACTGAGAGAGAGGGGGGGGGGGGAGAGGAGGA 805 11	OY 806 TTHATRONTTECCCTAMANATTETGRACCTCGTGATCCTAMAGGCCTNIACATE 865 121 THING THING THE THING THE THING THE THING THE THING THE THE THING THE THING THE THING THE THE THING THE THE THING THE THING THE THING TH	Oy 866 GCNCOTHCHGGAAGATTAAAGGTTCACTGGAATTGATCATCCATACGAACCACTA 925 1181 GACGGCAAGGAAGATTAAAGGTTTCACTGGAATTGATCATACATA	ATGGTGAGATAGTAATAAGATGAGAAAGAGAGAGAG	Oy 986 AACCAMCTICTATCCTACCTGAAGAAAACGGATATTGCAAGCTTAGTAATTTT 1045 1	Oy 1046 GAGAGATTGATCTTGTGTGTGCATTACTTGTGGACAGARTAGATCTGTTGT 1105  10	OY 1106 GGTCACATGANTAAAAGCATCAACATGAAGAAGAACAACAAGGGTCGGGTCATTCACA 1165  146GCATGAATAAAAGCATCAACAATAAACAATAACAAGAGCCACATTGATAGAA 472	Oy 1156 AACSGARAYGGATTCATTCAA 1190  Db 473 ACGGARACGARTATTCTTCA 497	RESULT 6 BF48112	LOCUS BF484142  LOCUS BF484142  BEFINITION WHEL188_GIO_ROUSE Wheat pre-archibets apike cDNA library Triticum	ACCESSION REveal of Course Clube Wall/OG_CIU_MAN, Sequence. VERSION BREVAIA2.1 GI:11567443	WS.	Spermachylar Masollophyta; Liliopsida; Poales; Pooldese Spermachylar Masollophyta; Liliopsida; Triticese Triticum; REFERENCE I (bases I to 421). AUTHORS Anderson, O.D., Chho, S., Cho, D. M., Close, T. J., Fenton, R. D., Man		genomes - Pre-anthesis spike cDNA library JOURNAL Umpoblished (2000) CONTRACT OF A CON		Tel: 5105959773 FRX: 510595618 FRX:	osydence have been thammou or senore vector adyonice and toward the source that phreed score less than 20
Db 61 NTATCTCCATACAGGAGAGATCCTGATGCATGCCGTGCTCTACTTCCAGATTCTAACTTT 120	Oy 797 ATTGAMGTATTATTGATTGCCCTAAAATTTGTGAAGCTGGTGATCCTAAAGGCCTA 856 121 ATTGAMGTATTATTGCCCTAAAAATTTGTGAAGCTGGTGATCCTAAAGGCCTA 856 bb 121 ATTGAMGTATTTGCCCTAAAAATTGTGAAGCTGTGAACCTGTGAAGCTGTAAGGTGG 180	09 857 TACABCTTCCACCTACACAMAGATTAAACGTTCACTCACAATTCATCACCACACACAA 916 Db 181 TACAMGCTTCACCCACACAAAAATTAAACGTTTCACTCACAATTAATCACTCAC	09 917 CONCOMPTRANTENDESTRANDISTRANDISTRANDES AND STREET CONCORNA 976 DD 241 COGCONTINITION OF THE CONTINUE OF THE CONCORNA 300	99 977 GANTGGGANGTTGTNFGGTAGGTTGAAGAAAGGGATTTGGAAGCTTAGTAT 1036  Db 301 GGANTGGGAAGCAGTTGTNFGCTTGAAGAAGGGATTTTGGAAGGTTAGGA 360	Oy 1037 ACMATTTGGGAAAATAACCGGTCCTTGGGCCCCATACTGGGCACACAACAAAA 1096 Db 361 ATATTGGGAAAATTGACCTGATTGTGGGCGCAATACTGGGGCAATACTAGAAA 117	ON 1997 TETETTOTTGGTCACTACATCAAAAAAACATCATAGGAAGTAACAAGTAACAGTACGGT 1156 Db 418 TCTGTTGGCCATGAATAAAAGGATCAACAAAAAAAAAAAAAA	09 1157 TCATCAGAMACGGARATGGARTCCCTTTAA 1190  Db 473 TGATCAGAMACGGARATCATTCATTGATTCA 506	a a	D. 25.26.91_A002 Dark Grown 1 (DG1) Sorghum blco sequence. BESS187 Communication of the process	S		AUTHORS Cordonnier-Pratt, MM., Gingle, A., Warsala, C., Sudman, M. and Pratt, mysty h. Profit Analysis Construction of the control of the c	TOWNEYT UNPUBLISHED (2000) COMMENT CONTEXT: CONFORMER PEACE, NA COMMENT CONFORMER FREEL NA COMMENT COM	The University of Georgia Plant Schences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 708 542 1860	Fax: 706 42.1805 Eaal: mmprattuga_edu Egaline mmprattuga_edu Sequences have been trimment to exclude PolyA, vector and regions below Phred quality 16. 7he threshold for hindnest quality sequence	is 20. Seq Piner: PolyTWix High quality sequence start: 64	High quality sequence stop: 697 PEATHRES Location/Gualifiers	rce	/Alone_libe^Tabak Grown   (108)  /Alone_bragns   5-day-old dark grown seedlings; Wactor: Lambda Zap; Site_1; XhOi; Site_2; E-copf; The library was made from Alone Nam in the cloning werene lambda 220 TR	Clones to be sequenced vere prepared by mass excision.

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BG873962 59-MAY-2001
MEST44-F08.T3 ISUM4-TN Zea mays cDNA clone MEST44-F08 3', mRNA
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clade; Pantochiese; Andropogonese; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: root; Vector: pBlueScriptII SK+; Site_l:
EccRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
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Qiu.F., Cui.F., Guo.L., Ashlock, D.A, Wen, T.J. and Schnable, P.S.
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/db.xref=-taxon:4577-
/closin=lib=-db.da - root cDNA library from Welbot Lab*
/tissue_tape="root"
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clade; Panicoldeae; Andropogoneae; 2ea.
1. (bases 1 to 627)
Walbot,V.
Malzo ESTS from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                               Contact: Walbot V
Departer of Balological Sciences
Starter of University
855 California Ave. Palo Alto, CA 94304, USA
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Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614077 row: E column
Location/Qualifiers
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r: Stratagene SK primer.
Location/Qualifiers
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Will, T.E. Elilab. Town. C.D., Bowman, C.L., Cravel, M.B., Ransen, T.S.,
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ESPE from roots of Medicago truncatula after incolubiton with
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propublished (1999)
Contact: Carroll P. Vance
Contact: Carroll P. Vance
University of Minnesota
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Programmed Sequence Geograms of State Seedlings and Silks (Purphilshed 2001). The Second Security Patrick S. Schnable Seconds to Patrick S. Schnable Seconds to Patrick Seconds Security Constitution Seasons Season Season Season Season University, Amer. 17 50011-1010, USA GOOD SEASON SEASON
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Pred. No. 3.5e-37;
0; Mismatches 7; Indels 0;
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Location/Qualifiers
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                   Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@lastate.edu
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1 (bases I to 772)
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Deviciopene for a genetically and physically anchored SST resource for bariety general sinorex drought-attessed seedling shoot chan.
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University Genomics Institute (CUGI) (Abgum, Palmer.
Tatsch, Atkins and Wing). Plasmid DNA preparations, DNA
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WvDMN0002 (Dehydration stress)"
/tissus_tpp="Seedling shoot"
/lab_host="TyGill"
417 GCCGCGCATTATTGCCAGATAAAAAGTTCATTGAGGTTTTTATGAATATGCCTCTACAAC 476
                                                                                       828 TITIGIGAAGCTCGIGAIGCTAAAGSCCIATACAAGCTIGCACGIACAGGAAGAITAAAG 887
                                                                                                                                  888 GTTCACTGGAATTGATGATCCATAGGAACCACAATTAATGGTGAGATAGTAATTA 944
517 GTTTAATTGATGATGATGATGATGAACTAGTGAGGATGATTAGATGGTGAGGATGATTA 513
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On Der 19. 2000 this sequence version replaced gill1895534
Comment of Markety General sestitute
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Total hq bases = 462
Seq primer: AFTAAACCCTACTAAAAGGG
High quality sequence stop: 675.
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/db_xref="taxon:4513"
/clone="HVSMED0015L17f"
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                                           BM407099 714 bp mRNA linear EST 22-JAN-2002
EST581426 potato roots Solanum tuberosum cDNA clone cPR029H6 5' end
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Abtrildae; euastardis I; Solanales; Solanaceae; Solanum.
I (bases 1 to 714)
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Teterback, T., Chlemingo, A., Bougri, O., Buell, C.R., Roming, C.,
Tanksley, S. and Baker, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 GITCAGGGAANAGINCICTIGCAIGTGCACTGAGTGGTGAGTTGCATTGCAGAGGCCACC 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contact Research Genetics, Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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pred. No. 3.3e-32;
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/Glone="prepare toots"
/Glose_lbr-potato roots*
/Glose_tbr-potato roots*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For clone info: please contact Research Genetics,
Division tel 1-800-711-6195, email cdna@resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Research Genetics, Libraries Division
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/cultivar="Kennebec"
/db_xref="taxon:4113"
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Best Local Similarity 70.6%;
Matches 379; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Solanum tuberosum
                                                                                                                                  mRNA sequence.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compus	protein search, using sw model	November 2, 2002, 00:28:47 ; Search time 50 Seconds (without alignments) 761.966 Million cell upda	-720-384A-4 HPINOTEPLVTHT00PP	BLOSUM62 Gapop 10.0 , Gapext 0.5	747574 seqs, 111073796 residues	of hits satisfying chosen parameters:	length: 0 length: 2000000000	Post-processing: Minimum Match 08	Listing first 45 summaries	A_Geneseq_032802:*	. /S1DS1/gcgdata/geneseq/genesepp-embl/AA1981.DAT: * 2. /S1DS1/gcgdata/geneseq/genesepp-embl/AA1981.DAT: * 3. /S1DS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: *	/SIDSI/gcgdata/geneseg/geneseg /SIDSI/gcgdata/geneseg/geneseg /SIDSI/gcgdata/geneseg	/SIDSI/gcgdata/genesed/genesed/ /SIDSI/gcgdata/genesed/genesed/ /SIDSI/gcgdata/genesed/genesed	/SIDS1/gcgdata/geneseq/geneseq /SIDS1/gcgdata/geneseq/genese	/SIDSI/gcgdata/geneseq/genese	/SIDSI/gcgdata/geneseq/genese	/SIDSI/gcgdata/geneseq/genese	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*	he number of results predicted	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES		h Length DB ID	343 21 224 21	311	208 21 259 21 272 21	7 251 21 AAG11017 7 251 21 AAG38348 7 263 21 AAG11016 7 963 21 AAG11016
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                                                                                                                                              New nucleic acid molecule and chimeric gene encoding an adenosine-5' phosphosulfate kinase, useful for altering expression of sulfate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.6%; Score 887; DB 21; Length 224; 77.0%; Pred. No. 2.8e-79; tive 16; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                         Claim 6; Page 29-30; 42pp; English.
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Falco SC, Allen SM,
                                                       WPI; 2000-182430/16.
N-PSDB: AA250159.
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Rest Local Similarity
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*Prospho-adenostare's phosphosulphate; RABS; sulphate assimilation; 
ozm. clono: cenin.pk0088.bJb; transgenic plant; screen; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1826; DB 21; Length 343; 100.0%; Pred, No. 7,9e-172;
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                              Claim 6; Page 31-32; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 SYILDGDNIRHGLNQDLSFRAEDRSENIRRIGEVAKLFADAGVICITSLISPYQKDRDAC 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 KDEECPSPKAMAKQVLCYLEENGYLQA 343
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05-MAR-1999;
09-MAR-1999;
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Flosspin-adenosine-5'phosphosulphate; PRPS; sulphate assimilation; 
sorybean; kinos spb2c.pk013.all; transgento pkant; screen; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 EKPVMSNIGKSTNILMHNCLIGOSDROKLLGORGCVVWITGLSGSGKSTLACALSRELHC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 RGHLTYILDGDNLRHGLNRDICFEAKDRAENIRRVGEVAKLFADAGLICIASLISPYRSE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 RGHLTYVLDGDNLRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 RDACRALLPHSNFIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 RSACRILLINSFEIEVPLAVPLEVCEARDPKGLYKLARAGKIKGFTGIDDDTVEAPADGDCT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                             New nucleic acid molecule and chimeric gene encoding an adenosine-5' appoprientiface kinase. vageful for altering expression of sulfate assimitation profesin in plants
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76.7%; Pred, No. 2.3e-76;
Live 24; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 VIKMKDEECPSPKAMAKQVLCYLEENGYLQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 VIOCKAGDCATPKSMADOVVSYLBANPELO 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                  Allen SM. Anderson SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 35; 42pp; English.
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ication; signal transduction pathway; metabolic pathway; VRHGLNRDLSFKAEDRAENIRRYGEVAKLFADAGIICIASLISPYRTDRD 172 DGR------GARTHCHRGIGRWVRRRRRNGAAPGEAPHSPVKEK 134 LRHGINRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRD 254 FIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGELVI 314 44.74; Score 817; DB 21; Length 259; Lty 60.64; Pred. No. 2.8e-72; Endela 22; Gaps servetive 32; Mismitches 52; Endela 22; Gaps NSRSVVVVRACVSMDGSQTLSHNKNGSIPELKSING------HTGQKQG 53 liana protein fragment SEQ ID NO: 14354. KAMAKOVLCYLEBNGYLQA 343 rd; Protein; 272 AA irst entry)

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Protein identification; signal transduction pathway; metabolic pathway; 
hybridisation assay; genetic mapping; gene expression control; promoter; 
decemination sequence.
                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 9573.
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13-AUG-1999; 9	-AUG-1999;	-AUG-1999;	8-AUG-1999;	J-AUG-1999;	- 906-1999	-AUG-1999;	-AUG-1999;	5-AUG-1999;	5-AUG-1999;	-AUG-1999;	-Aug-1999;	-Aug-1999;	- AUG-1999	-SED-1999:	-SEP-1999;	)-SEP-1999;	8-SEP-1999;	-SEP-1999;	5-SEP-1999;	1565T-1365	- CED-1999;	- CED-1999;	- SED-1999	-SED-1999;	-OCT-1999;	5-OCT-1999;	5-0CF-1999;	1-0CT-1999;	3-OCT-1999;	2-0cT-1999;	-OCT-1999;	2-OCT-1999;	-OCT-1999	-OCT-1999:	1-OCT-1999;	1-OCT-1999;	1-OCT-1999;	-Oct - 1999;	1-0CT-1999:	1-OCT-1999;	1-OCT-1999;	1-OCT-1999;	1-OCT-1999;	-001-1999;	2-OCT-1999;	5-OCT-1999;	5-OCT-1999;	5-OCT-1999;	5-OCT-1999;	5-0CT-1999;	8-0cT-1999;	8-OCT-1999;	8-OCT-1999;
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QY 100 GARTHCHRGIGRWYRR             18 GSQTLSH	RRRNGAAPGEAPHSPVKEKPVMSNIGKSTNILMHNCLIGQS 156		-NKNGSIPEVKSINGHIGOKOGP-LSTVGNSTNIKWHECSVEKV 66
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157 DRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLDGDNLRHGLNRDLSFK 216 Gaps 44.7%; Score 816; DB 21; Length 251; 64.4%; Pred. No. 3.4e-72; 1ve 32; Mismatches 40; Indels 16 32; Mismatches

Protein identification; signal transduction pathway; metabolic pathway; Proteinstion assay; genetic mapping; gene expression control; promoter: termination sequence. Arabidopsis thaliana protein fragment SEQ ID NO: 9572 AAG11016 standard; Protein; 263 AA. 17-0CT-2000 (first entry) 337 ENGYLOA 343 245 NKGYLQA 251 AAG11016; RESULT 10 AAG11016 ò 6

Arabidopsis thaliana EP1033405-A2.

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Query Metch   Maintay   44,71, Score 816; DB 21; Length 233;	217 ARTICLEM TENDER TO THE TABLE TO THE TABL	388	As Analogues telaliana.  Manager Sept. 2000.  Manag	14-MAY-1999;

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Protein identification; signal transduction pathway; metabolic pathway; 
Pyytidsation assay; genetic mapping; gene expression control; promoter: 
termination sequence.
                                                                                                                                                                      10 GARTHCHRGIGRHVRRRRRNGAAPGEAP---HSPVKEKPVMSNIGKSTNILMHNCLIGOS 156
                                                                                                                                                                                                                    157 DRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLDGDNLRHGLNRDLSFK 216
                                                                                                                                                                                                                                    79 DRQRLLDQKGCVIWVTGLSGSGKSTLACALNQMLYQKGKLCYILDGDNVRHGLNRDLSFK 138
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                                                                                                                                                                                                                                                                                                                                        199 CEARDPKGLYKLARAGKIKGFTGIDDPYEPPLNCE--ISLGREGGTSPIENABKVVGYLD 256
                                                                                                                                            40; Indels 16; Gaps
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64.4%; Pred. No. 3.7e-72;
tye 32; Mismatches 40; Indels 1
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990S-0161406.
99US-0161359.
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                                                                                                                                Best Local Similarity 64.4%:
Matches 159: Conservative
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hypridisation assay; genetic mapping; gene expression control; promoter; 
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Query Match

44.7%; Score 816; DB 21; Length 276;

Best Local Similarity 64.4%; Pred. No. 3.96-72;

Matches 159; Conservative 32; Mismatches 40; Indels 16

Matches 159; Conservative 32; Mismatches 40; Indels 16
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FastSEQ for Windows Version 2.0
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3174 Porter Drive
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FILING DATE: Herewith
CLASSIFICATION: 424
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Patent No. 5817482
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ATTORNEY FAGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET NEUBER: PF-07
TELECOMBUNICATION INFORMATION:
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IBM Compatible
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LENGTH: 610 amino acids
TYPE: amino acid
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CITY: Palo Alto
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| Application | 
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                                                                                                                                                                         November 2, 2002, 01:49:58; Search time 19 Seconds
(without alignment)
440.946 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summeries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1826
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STRANDEDNESS: single

POPOLOGY:

; IMMEDIATE SOURCE: ; LIBRARY: GenBank ; CLONE: 705385 US-08-879-561-10

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26; Gaps

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Matches 106: Conservative 38: Mismatches 60: Indels
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                                                                                    143 STNILWHNCLIGGSDRQKLLGQ----KGCVVWITGLSGSGKSTLACALSRELHCRGHLTY 198
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                                                Gaps
                                                                                                            10 ATNUTEOTOHVSRAKRGOVLGORGERGCTWPTGLSGAGKTI1SFALEBYLVSGGIPTY 69
                                                21;
Ouery Match
Bast Local Samilarity 47.3%; Score 502.5; DB 2, Length 610,
Bast Local Samilarity 47.3%; Fred No. 6.16.43
Retches 2.13, Indebs 21,
Retches 103; Conservetive 34; Mismatches 51, Indebs 21,
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THILD OF TAWARTICH DISABLE RELATED NUCLEOTIDE KINASES
NUMBER OS SEQUENCES. 1
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APPLICATION NUMBER: US/08/879,561
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                        314 I --- KMKDEECPSPKAMAKOVLCYLEENG 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0325 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08879561
Patent No. 5817482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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IBM Compatible
SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TELEPAX: 415-845-4166
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TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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PRIOR APPLICATION DATA:
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LIBRARY: LUNGNOT02
CLONE: 373887
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OPERATING SYSTEM:
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125 BAPHSPVKEKPVMSN----IGKSTNILWHNCLIGQSDRQKLLGQ----KGCVVWITGLS 175
                                                                                                                                                                                    176 GSGKSTLACALSRELHCRGHLTYVLDGDNERHGLNRDLSFKABDRAENIRRVGEVAKLFA 235
                                                                                                                                                                                                                                             62 GAGKTTVSMALEEYLVCHGIPCYTLDGDNIRQGLANNLGFSPEDREENVRRIAEVAKLFA 121
                                                                                                                                                                                                                                                                                                                                                                         236 DAGVICIASLISPYRRDRDACR-----ALLPHSNFIEVFIDLPLKICEARDPKGLYKLAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                  112 DAGLUCITSFISPYTQDRNNARQIHEGASLP---FFEVFUDAPLHUCEQRDVKGLYKKAR 178
                                                         2 EIPGSLCKKVKLSNNAQNWGNQRATNVTYQAHHVSRNKRGQVVGTRGGPRGCTVWLTGLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 TGKIKGFIGIDDPYEPPINGEIVIKMKD---EBCPSPKAMAKOVLCYLEE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 AGEIKGFTGIDSEFEKPEAPELVEKTDSCDVNDC-----VQQVVELLQE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 495; DB 2; Length 624; 46.1%; Pred. No. 3.7e-42;
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SOFTWARE PRESENT OF Windows Version 2.0
CURRENT APPLICATION DATA:
FILLEN PARM
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Palo Alto
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Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08879561
Patent No. 5817482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
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LENGTH: 624 amino acids
TYPE: amino acid
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TELEFAX: 415-845-4166
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
Matches 106: Conservat
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CLONE: 1109676
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Gaps 56:

Indels

Mismatches

38:

Conservative

Score 495; DB 2; Length 624; Pred. No. 3.7e-42;

27.1%;

Query Match Best Local Similarity

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174 SDALLPLHPAVIGADT-----LFRQSEMEGETNDARRRESIWST----AGRK--- 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 HGLTPRSSHSSAGLASDSGRREGEGRGARTHCHRGIGRW-VRRRRRNGAAPGEAPHSPVK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 --TTRRSAHS-------WPLTSLRTASSAPGSATRGECC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 EKPVM----SNIGKSTNILWHNCLIGGSDRQKLLGGKGCV----VWITGLSGSGKSTLA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 CALSRELHCRGHLTYVLDGDNLRHGLNRDLSFKAEDRAENIRRV-----GEVAKLF- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 PSPAPGPASGG-----ORGGNTLLSPTPTLAVILVNPQRAPPVLPGLTPSD-APLPALVI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de Lange, Titta
APPLICANT: SHith, SUSAN
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TREI AND METHODS
TITLE OF INVENTION: OF USB THEREDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 5.3%; Score 96.5; DB 4; Length 620; Best Local Similarity 23.3%; Pred: No. 0.23; Best Local Similarity 23.3%; Signature 30; Mismatches 65; Indels 10 Matches 61; Conservative 30; Mismatches 65; Indels 10
                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
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: 411 Hackensack Avenue, 4th Floor
Hackensack
                                                                                                                                                                                                                                                                                                      SOCTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/411,111
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US-09-196-8 Application US/09196387

Squence 8. Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
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                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 4
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CORRESPONDENCE ADDRESS:
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          COUNTRY:
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125 BAPHSPVKEKPVMSN----IGKSTNILWHNCLIGQSDRQKLLGQ----KGCVVWITGLS 175
                                                                                                                                                                                                176 GSGKSTLACALSRELHCRGHLTYVLDGDNLRHGLARDLSFKAEDRAENIRRVGEVAKLFA 235
                                                                                                                                                                                                                                                   62 GAGKTTVSMALREYLVCHGIPCYTLDGDNIRGGENKNLGFSPEDRERVYRLAEVAKLFA 121
                                                                                                                                                                                                                                                                                                                                                                                                 236 DAGVICIASLISPYRRDRDACR-----ALLPHSNPIBVFIDLPLKICEARDPKGLYKLAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 5.34; Score 97.5; DB 4; Length 655; Best Local Similarity 27.54; Pred. NO. 0.2, Matches 48; Conservative 11; Mismatches 62; Indels 43; Gaps
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                                                            2 BIPGSLCKKVKLSNNAQNWGMQRATWVTYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLS 61
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APPLICANT: TOC. WILE
APPLICANT: TOC. WILE
APPLICANT: TANG. SHOP
APPLICANT: SH
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APPLICARY: Famed, LAYO,
APPLICARY: Famed, LAYO,
TITLE OF INVENTION: Rectors involved in Gene Expression
FILE REPERENCE: BR-1172
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CURRENT FILMO DARE: 1939-0-02
EMBLIER APPLICATION NUMBER: 60/092.415
EMBLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 11
SOFTWARE: MICROSCH OFFICE 97
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1155 Avenue of the Americas
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Patent No. 6359193
GENERAL INFORMATION:
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Patent No. 6294658
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STREET: 13
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US-09-347-833-4
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APPLICATION NUMBER: US/09/196,387
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                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
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                                                                                                                 Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201-343-1684
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US-09-196-387-10
                                                               ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
    Hackensack
New Jersey
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                                                 USA
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                                                 COUNTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 SSSPTSSSSSSPSSPGSSLAESPEAAGVSSTAPLGPG------AAGPGTG----- 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%; Score 96.5; DB 4; Length 673;
20.2%; Pred. No. 0.26;
ive 34; Mismatches 143; Indels 131; Gaps
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TREI AND METHODS
TITLE OF INVENTION: OF USE THEROF
                                                                   SOFTWARE: Patentin Release 41.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                        600-1-230 CIP1
                                                                                                                 APPLICATION NUMBER: US/09/196,387
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGBNT INFORMATION:
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Patent No. 6277613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 913-1684
TELEFAX: 133521
INFORMATION FOR SED ID NO: 8: SEQUENCE CIPARACTERISTICS:
LENGTH 573 small o acids
TIPE: amain acid
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TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
US-09-196-387-8
                                                                                                                                                              CLASSIFICATION .
                                                                                                                                       PILING DATE:
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US-09-196-387-10
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72 RDPDDRPRSPDPVDGTSCCSTTSTICTVAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSS 131
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PEPLICANT: Smith, Suame PROTEIN THAT BINDS TO TREI AND METHODS
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TREI AND METHODS
COMPUTER: IBM PC compatible
OPERATINS SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/GENT INFORMATION:
NAME: Dackson Est, David A.
REGISTRATION NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 600-1-230 CFP1
TELECOMOUNICATION INFORMATION:
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US-08-884-072-3
; Sequence 3, Application US/08884072
; Patent No. 5872234
                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 RPVMSNIGKSTNILMHNCLIGGSDRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 NACS--FGHABVVS-----LLLCQGADPNARDNWNTTPLHEAAIKGKIDVCIVLLQHGA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 -----APLPALVIHGLTPRS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 RDPPDRPRSPDPVDGTSCCSTTSTICTVAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 SHSSAGLASDSGRREG -----EGRGARTHCHRGIGRWVRRRRRNGAAFGEAPHSPVKE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 VPAVSG---ALRELLEACRNGDVSRVKRL------VDAANVNAKDMAGRKSSPLHFA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .94 GHLTYVLDGDNLRHGLARDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRDR 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 DACRALLPHSNFIEVFIDLPLKICEARDPKG-----LYKLARTGKIKGFTGI---D 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 HHQQLQP-APGASAPPPPPPLSPGAPGTTPASPTASGLAPFASPRHGLALPEGDGS 71
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20.2%: Pred. No. 0.7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                        5: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/196,387
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                  TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 20.2%
Matches 78; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             CIFY: Hackensack
STATE: New Jersey
COUNTRY: USA
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83 ATPLOQEKLLPAQLPAEKEVGPPLPQEAVPLQKELPSLQHPNEQKEGMPAPFGDQSHPEP 142
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RAFLOKAN BRADADA (OLGA
PAPLICANT COLGAY MRII C.
PAPLICANT COLGAY MRII C.
PAPLICANT CORGANI CONTROLLINIAR MATRIX PROTEINS
THILE OF THERETON BENDERAL STATE OF THE 
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,072
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TELEPHONE: 415-855-0555
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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LENGTH: 540 amino acids
TYPE: amino acid
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FILING DATE:
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CLONE: 1621777
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65 DAPLPALVIHGLTPRSSHSSAGLASDSGRREGEGRGARTHCHRGIGRWVRRRRRGAAPG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 EAPHSPVKEKPVMSNICKSTNILMHNCLIGQSDRQKLLGQKGCVVWITGLSGSGKSTLAC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638 DREYYOLVSKELLRNV-----STITPKGKLTMVIGSTGSGKSTLLG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 AL-----SRELHCRGHLTYVLDGDNLRHG-LNRDLSFKAEDRAENIRRVGEVAKLFAD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    679 ALMGEYSVESGELWAERSIAYVPQQAWIMNATLRGNILFFDEERAEDLQDVIRCCQLEAD 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 AGVIC-----IASLISPYRRDR-DACRALLPHSNFIBVFIDLPLKICEARDPKGLY 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 : | : | : | : | : | 39 LAOFCGGLDTELGEMGVNLSGGGKARVSLARAV--YANRDVYLLDDPLSALDAHVGORIV 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 21.3%; Pred. No. 1.2;
Matches 54; Conservative 41; Mismatches 101; Indels 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.2%; Score 95; DB 1; Length 1548;
21.3%; Pred. No. 1.2;
                           CORRESPONDENCE ADDRESS:
ADDRESSER: PARTEO RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen'S University at Kingston
                                                                                                                                                                                                                                                                       SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/U8/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 436
                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/966,923
FLING DAFE: 27-0CT-1992
CLASSIFICATION: 435
REIDER APPLICATION DATA:
APPLICATION NUMBER: 08/029.340
FILING DATE: 8 *MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/407,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Steeg, Carol Migrnicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 0154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/40
FILING DATE: 20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY / AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 KLARTGKIKGFTGI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797 QDVILGRLRGKTRV 810
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
         NUMBER OF SEQUENCES:
                                                                                                                     STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                   Kingston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-463-092B-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 ATPLOGEKLLPAGLPAEKEVGPPLPGEAVPLQKELPSLQHPNEQKEGNPAPFGDQSHPEP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 EGRGARTHCH--RGIGRWVRRRRRNGAAPGEAPHSPVKEKPVMSNIGK----STNILWH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 ESWNAAQHCQQDRSQGGW--GHRLDGFPPG-----RPSPDNLNQICLPNRQHVVYG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 RPEHFQEVGYAAPPSPPLSRSLPM----DHPDSSQHGPPFRGQSQ----9QPPPSQB--- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 VNPQRAPPVLPGLTPSD----APLP--ALVIHGLTPRSSH---SSAGLAS---DSGRREG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RPFHF------INQTEPLVTHTQQPPSPAPGPASQGQRQGNTLLSPTFLAVIL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COLO, SUBBAR P.C.
APPLICANT: COLO, SUBBAR P.C.
TITLE OF INVENTION: ISOLATED WILLIDRUG RESISTANCE PROPERNS
TITLE OF INVENTION: MULTIRUG RESISTANCE PROPERNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.2%; Score 95; DB 4; Length 540;
23.0%; pred, No. 0.27;
APRICANY: Bandam, Olipa
PARICANY: Conjey, Meli C.
PARICANY: Conjey. Tall J.
TITLE OP. TRIBENTO II. BURNA EXTRACELLULAR MATRIX PROTEINS
NUMBER SEQUENCES. SEQUENCES:
ADMESSED Indep Parimenticals, Inc.
STREET: 3114 perter prive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 NCLIGQSDRQKLLGOKGCVVWITGLSGSGKSTLACALSRELHCRGH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 PWNLPQSSYSHLTRQ-----GETLNFLEIGYSRCCHCRSH 226
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA: US/09/212,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.0%; pred. No. 0.27;
Matches 52; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTACHEN PAREN.

NAME: BILLINGS, Lucy J.

RECISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0333 US

TELECOMKUNICATION INFORMATION:

TELECOMKUNICATION: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/884,072
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Patent No. 5766880
                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 540 anino acids
TYPE: amino acids
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
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LIBRARY: BRAITUT13
CLONE: 1621777
                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                                                                                                         Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                         94304
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                                                                                                                                                                                                                                  COUNTRY
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                                                                                                                                                                                                                STATE:
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8

Gaps

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739 LAQFCGGLDTEIGEMGVNLSGGGKARVSLARAV-YANRDVYLEDDDFLSALDAHVGGRIV 796
679 ALMGEYSVESGELWAERSIAYVPQQAWIMNATLRGNILFFDEERAEDLQDVIRCCQLEAD 738
                                                                                        237 AGVIC-----IASLISPYRRDR-DACRALLPHSNFIEVFIDLPLKICEARDPKGLY 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 APLPALVIHGLTPRSSHSSAGLASDSGRREGEGRGARTHCHRGIGRWVRRRRRNGAAPGE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 OPAP-----TPSVGSSFFSSLSQAVKQTAASAGLVD------APAP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 APHSPVKEKPVMSNIGKSTNILWHNCLIGQSDRQKLLGQKGCVVWITGLSGSGKSTLACA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Indels 61; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Greenpart, Paul
APPLICANT: Greenpart, Paul
APPLICANT: ROTION, BALDER
TITLE OF INDEXTOR: NO MUST THE BORONING THE HUMAN STWAPSIN III GENE
THE OF INDEXTOR: NO NESS THERROY
CORRESPONDERS: NO NESS THERROY
CORRESPONDERS
CORRESPO
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5.23: Score 94.5; DB 3; Length 582;
Best Local Similarity 22.84; Pred. No. 0.34;
Matches 49; Conservative 20; Mismatches 85; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: David A. Jackson, Esg.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
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TOPOLOGY: Linear
HOLBCULE TYPE: protein
DESCRIPTION: /desc = 'Synapsin IIa"
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APPLICATION NUMBER: US/08/906,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
WEDIUM TYPE: Flopy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 3, Application US/08906865
Patent No. 6040168
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                   287 KLARTGKIKGFTGI 300
                                                                                                                                                                                                                                                                                                                                                                                      797 ODVILGRIRGKTRV 810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-906-865-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-906-865-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 DAPLPALVINGLTPRSSHSSAGLASDSGRREGEGRGARTHCHRGIGRWVRRRRRNGBAPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 DASASSLAVHSTTVHMG-STQTVITDSDGAAGED------EKGEVEEG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 EAPHSPVKEKPVMSNIGKSTNILWHNCLIGQSDRQKLLGQKGCVVWITGLSGSGKSTLAC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 DREYYQLVSKELLRNV------STIPKGKLIMVIGSTGSGKSTLLG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 101; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.2%; Score 95; DB 2; Length 1548; Best Local Similarity 21.3%; Prefd. No. 1.2; McHorles 54; Conservative 41; Mismatches 101; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEO RESEARCH & DEVELOPMENT INNOVATIONS
                                                                                                                                                                                                                                                                         APPLICANT: Dealey, Roger G.
APPLICANT: Ocle, Nasan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Queen's University at Kingston
CITY: Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 444
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 404
ATOMSEZ/ADRA: 1959
RATING DATA:
RADA: 2049

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: ASCII tovt
                                                                              US-08-460-907B-7

SEQUENCE 7, Application US/08460907B

Patent No. 5891724

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 424
PRRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 424
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1548 amino acids
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FRAGMENT TYPE: internal
US-08-460-9078-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Flopov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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K7L 3N6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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106 APAAARKAKULL--VVDEPHADMAKCFRG----KKULGDVDIKVROAFFS------149
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                                                                                                                                                                                                                           PRICHENT BY SPRIZED

PRICHENT INFORMATION

APPLICANT: MINISTER

APPLICANT: SERVE APPRICANT

APPLICANT: DUTLOW, PARRICE

APPLICANT: DUTLOW, PARRICE

THE OF TREPATION: SPRIMENTATION PARTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM YTRE: Floppy disk
COMFOTER: IBM PC Compatible
COMPANTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                             186 LSRELMCRGHL -- TYVLDGDNLRHGLNRDLSFKAE 218
                                                                             150 ---ELNLVAHADGTYAVDMQVLRNGTKVVRSFRPD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/815,718
                                                                                                                                                                                                              Sequence 2, Application US/08815718
Patent No. 5981220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 415 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein
US-08-815-718-2
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                               97 EGRGARTHCH--RGIGRWVRRRRRNGAAPGEAPHSPVKEKPVMSNIGK-----STNILMH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                             143 ESWAAQHCQQDRSQGGW--GHRLDGFPPG------RPSPDNLNQICLPNRQHVVYG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 NCLIGQSDRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCRGH-----LTYVLDGDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 PWNLPQSSYSHLTRQ-----GETLNFLEIGYSRCCHCRSHTNRLECAKLVWEDT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 LRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRALLPHSN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                    1 RPRHF------INQTEPLVTHTQQPPSPAPGPASQGQRQGNTLLSPTPTLAVIL 48
                                                                                                                                                                           1 | | | | 34 RPBHFQEVGXAAPPSPPLSRSLPM ----DHPDSSQHGPPFEGGSQ---- 82
                                                                                                                                                                                                                                                                 49 VNPORAPPVLPGLTPSD----APLP--ALVIHGLTPRSSH-----SSAGLASDSGRRBG 96
                                                           Matches 64; Conservative 34; Mismatches 113; Indels 90;
5.1%; Score 94; DB 2; Length 415;
21.3%; Pred. No. 0.24;
      Query Match
Best Local Similarity
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APPLICANT: Rolzman, Bernard
APPLICANT: Liu, Fenyong
APPLICANT: Liu, Fenyong
TITLEON: Methods and Compositions of a
TITLE OF INVENTION: Preparation and Use of A Herpes Protease
                                                                                                                                                                                                                E: ARNOLD, WHITE & DURKEE
321 No. 5478727th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/07/832,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCD045
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   ; Sequence 2, Application US/07832855
; Patent No. 5478727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coolley, Ronald B. REGISTRATION NUMBER: 27,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312) 744-0090
TELERAX: (312) 245-4961
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 635 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19920207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein
US-07-832-855-2
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                 NUMBER OF SPOURNCES:
                                                                                                                                                                                                                        ADDRAGO
STREET: 324 .
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   60610
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RESULT 15
US-07-832-855-2
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43; Indels 11; Gaps Query Match 5:0%; Score 91.5; DB 1; Length 635; Dest Local Similarity 33.0%; Pred. No. 0.79; Matches 30; Conservative 7; Mismetches 43; Indels 1 Matches 30; Conservative 7; Mismetches 43; Indels 1

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Search completed: November 2, 2002, 01:54:10 Job time : 22 secs

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Compyright (e) 1959 - 200 Compagen Ltd.  ON protein - protein search, using sw model Run on: November 2, 2002, 001-51:22; Search Line 99 Seconds Fills: US-09-720-3844-4 Septice; Search Line 199 Seconds 1 PROFINGTREPATHTODPP	Searched: 283138 seqs, 96089334 residues Ortal number of hits settefring about assummations.	Cost number to III.s Satts17109 chosen parameters: 283138 MAIATIMA DE Seq length: 200000000 POST-PICOGESION INITIAM MACCO 1004 POST-PICOGESION MAIATIMA MACCO 1004	Database : 1735 4.5 summartee : 1735 4.5 summartee : 1735 7.5 summartee	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SERVET STORE DESCRIPTION TO THE PROPERTY OF TH	833 45.6 816 44.7 777 4 42.6 571 31.3 555 30.4 534 5 29.3 511.5 28.0	510 27.9 213 2 KP0408 508.5 27.8 625 2 K87433 505 27.7 652 1724918 503.5 27.6 502 1724918 503.5 27.5 610 1 204383 408.5 27.3 660 2 682672	77.1 201 2 A M10856 77.1 624 1 JW00856 77.2 25 2 F82062 76.9 644 2 AD3471 76.9 641 1 ZZZWNO 76.9 641 1 B65956 76.3 201 1 B65956 76.3 201 2 O91079	481 481 478.5 478.5 457 448.5 402

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Firebling J. Bercon. G. Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibelon, R.; I. S. Hebling, J. S. Bercon. G. Ometchenko, M.V.; Smith, D.R. J. Sengerio, 1814, 4623-4639, 3001

Antities Genome Requence and Comparative Analysis of the Solvent-Producing Bacterium Antities compare National 1915-1159355.
                 RiBeron, M.; Murphy, G.; Ridlay, P.; Hudaon, S.; Bantroft, 1.; Meres, H.W.; Mayer, audmitted to the Protein Sequence Detabase, March 1999
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A.Rasidoses: 1-200 «KUP»
A.Cross references: 01.00 «KUP»
A.Experimental source: Closeltidium acetobolylicom ATCO34
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BACE 18. Glaselmann, G.; Schliffmann, S.; Schwenn, J.D.
Bacchin. Biology, Sect. 2124, 474-521, 2364
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C:Speciaes Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
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54.9%; Pred. No. 1.7e-36;
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No. 1.7e
35: Mismatches
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A:Map position: 4
A:Introns: 78/1, 177/1; 216/3; 245/1; 260/3
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Matches 113; Conservative
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RiATE, H.E.; Gisselmann, G.; Schliffmann, S.; Schwenn. J.D.
Arittler & OOMA for ademylyl adiplate 1,894
Arittler & OOMA for ademylyl adiplate (AFS), 1894
Arittler & AOMA for ademylyl adiplate (AFS), Kinase from Arabidopsis thallana.
Arkocession: SUFG40, MOTD:94325585
Arkocession: SUFG40
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A:Residues: 1-276 <STO>
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Rivineani, III, Nakadone, K. Tatkaki, Y. Tatkano, G. Sasaki, R.; Mesti, K.; Puji, F.; R Yariki, Codie Res. 28, 4117-431, 2000 A Parkine Code se seque sequence adquence of the abaliphilic beterrium Bestillus halodurans a A Accession, 48395 MSGO, WIDGO, MID. 20125, PHID. 110933. A Nacienie (Vyein DNA. 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – 2014 – "Michigan desiron yalancha kanase (EZ 27.1.25) [Imported] - Sinorhizobium melijori (et Giber 2.5 Anno 270) teat. Character 2.5 A SECRET FOLLIANDS TO FOLLIANDS TO SECRET FOLIANDS TO SECRET C:Superfamily: nodulation protein nodO: adenylylsulfate kinase homology; translation C:Reywords: phosphotransferase ä C:Species: Bacillus halodurans C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001 Gabs 145 NILWHNCLIGQSDRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCRGHLTTVLDGDN 204 8 HIVWHEASVSKEERQKRNREKSCVVWFTGLSGSGKSTLANALDRKLPEGGIHSYVLDGDN 67 205 LRHGLNRDISFKAEDRAENIRRVGEVAKIFADAGVICTASLISPYRRDRDACRALIPHSN 264 68 IRHGLMAGLGFSEDRKENIRRIGEVAKLFVDAGVVTSTAFISPFREDBDNVRGILDDGE 127 265 FIEVFIDLPLKICEARDPRGLYKLARTGKIRGFTGIDDPYEPPINGEIVIKMKDEGCPSP 324 128 PIENVVROPIETCERRODENSIANE | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... Gaps C: Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology 2; ä DB 2; Length 202; Length 633; 58; Indels Indels Score 511.5; DB 2; Pred. No. 2.5e-31; 1.1e-33; ; Pred. No. 1.1e 28; Mismatches 29.3%; Score 534.5; 53.8%; Pred. No. 1.1e 24: Mismatches 28.0%; 325 KAMAKOVLCYL -- EENG 339 Best Local Similarity 53.8% Matches 106; Conservative 185 BEAVEKIYAYLHAOESG 201 Matches 101; Conservative Local Similarity A;Gene: nodQ2; SMb21224 A; Contents: annotation A;Status: preliminary C; Accession: A83836 A; Genome: plasmid BH1489 Query Match Query Match A: Gene: ò 6 à 8 ò g õ 8 Anstitute profilantary nucleic acid sequence not shown: translation not shown. Askelonie type: Nav Askelonie type: Nav Askelonie type: Nav (1991)09; GB:AL009126; NID:q5613260; PIDB:CAN12931.1; PID:q5633427 Anspeciational source: strain 108 ä adenylylsulfate kinase BH1489 [imported] - Bacillus halodurans (strain C-125) C:Species: Beclinas subtilis C:Species: Beclinas subtilis C:Date: 1997 #sequence\_revision 05-Dec-1997 #text\_change 19-Jan-2001 C:Accession: A69839 139 NIGKSTNILWHNCLIGOSDROKLLGOKGCVVWITGLSGSGKSTLACALSREHURGHITT 198 199 VLDGDNIRHGLURDLSFKARDRAENIRRYGEVAKLFADAGVICIASLISPYRRDRDACRA 258 62 LLDGDMLRYGLNSDLGFKSEDRTENIRRYSEVAKLFADAGIITITFISPPIEDRNNARR 121 259 LLPHSNFIBVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPVRPPINGFIVI---K 315 122 LL-GKDFVEVYIDCPIEVCERRDPKGIYKRARNGEIKNFTGIDSPYEKPEKPEITVETYK 180 145 NILWHNCLIGOSDROKLLGQKGCVVWITGLSGSGKSTLACALSRRLHCRGHLTYVLDGDN 204 205 LRHGLARDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRALLPHSN 264 6 NIIMHPAAISKSDRQSLNGHKSCVLMFTGLSGSGKSVLANAVDEKLYRKGIQSYVLDGDN 65 Gaps 265 FIEVFIDLPLKICEARDPKGLYKLARTGKIKGPTGIDDPYEPPINGELVIK 315 126 FFELYVKCPLHYCEQRDPKGLYKKARNGEIKHFTGIDSPYEAPLSPDFIIE 176 Length 199; 44; Indels adenylylsulfate kinase homolog yisz - Bacillus subtilis 2.9e-35; DB 2; 27; Mismatches 30.4%; Score 555; 58.5%; Pred. No. 2 316 MKDEECPSPKAMAKQVLCYLEENGYL 341 181 DIEEKC----VDNIIEYLKOHKIL 200 100; Conservative Similarity Query Match Best Local Si Matches 100; ò a ò 8 ð 8 g £ ð à Š

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C: Superfamily: nodulation protein nodO; adenylyisulfate kinase homology; translation
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Asbocanie 1652 481L5
Toross references: BMBL:26880; PIDN:CAA93098.1; GSPDB:GN0022; CESP:T14G10.1
Asbpetiamental Source: clone T14G10
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Affariate nasses: protein TA(10.1).
C.Species: Openorhabditis elegans
C.Species: 27-oct-1999 *Facture-central protein 270-oct-1999 *Facture-central control 
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                                                                                                                                                                                      64; Indels 16;
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submitted to the EMBL Data Library, January 1996
A;Reference number: 219954
A;Accession: T24918
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A; Introns: 23/3; 82/3; 176/1; 535/2; 623/2
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ò ò g \* A;Cross-references: GB:AE005673; NID:913422853; PIDN:AAK23461.1; GSPDB:GN00148

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arithe: The demone sequence of the plant pathogen Xylella fastidiosa. Abfacence number. A82515; MULD:20165717. Abfacence number A85928 below AnAccession: G86071
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N'Alternate manes: ademosine 5"-phosphosulfate kinase; PARS
N'Contains: ademylypiatiate kinase (EC 2.7.1.73); suifate ademylyltransferase (EC 2.7.7.7.
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C.Data. T.74ar.1996 Saquence_revision 19-Apr.1996 Ftext_change 19-Jan-2001
S.Accession: OC183
R.Rosenthal. E., Leustek. T.
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A.Residues: 1-fi(0 4705>
A.Cross-references: GB:L39001; NID:g705384; PIDN:AAB00139.1; PID:g705385
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C:Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
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A.Reference number: 225037
A.Reference number: 225037
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Arabidopsis Tabilana (Mosse-sar cress).

Bermatophyta; Mradiplantes Streptophyta; Embryophyta; Tracheophyta; Stematophyta; Marabidopsis oldophyta; Streptophyta; Orde addicts; Rosidae; Strestatoedes; Arabidopsis-uducosis; IR prassicalae; Brassiacaes, Arabidopsis-uducosis; Strestatoedes; Arabidopsis-uducosis; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 GARTHCHRGIGRMVRRRRRNGAAPGEAP---HSPVKEKPVMSNIGKSTNILMHNCLIGQS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 GSQTLSH-----NKNGSIPEVKSINGHTGQKQGP-LSTVGNSTVIKWHECSVEKV 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Werk-2000 (Bal. 3), Creekel)
30-HW-2000 (Bal. 3), Last sequence update)
30-HW-2000 (Bal. 3), Last sequence update)
Admin/1 market of the control of the cont
                                                                                                                                                                                              -1- PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | BEBL. 75792; CAS3465.11.
| BEBL. 187979.25 CAS3465.11.
| BEBL. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 276;
FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB698643AA09D811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               -- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.7%; Score 816; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
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                                                                                                                              phosphoadenylylsulfate.
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Matches 159; Conserv
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                                                                                                                                                                                                                                                                                      99 PGKKILOTTTVGNSTNILMHKCAVEKSENOEPLOORGCVINITGLSGGGKSTLACALSRG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota: Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; edicotyledons; core editoots; Rosidae;
enrosids II; Brassicales; Brassicaeee, Arabidopsis.
                                                                            Gaps
                                                                                                                                                                                                          130 PVKEKPVMSNIGKSTNILMHNCLIGOSDROKLLGOKGCVWJIGLSGSGKSTLACALSRE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 D. LHCBGHT, DYVI, DGDNI, BHGT, NRDT, SPKARDBARN TRRUGEVAKT, PADAGV TCTAST, TSPY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 IHANGKLTYTLOGDNVRHGLNSDLSFKARDBARNTRRIGEVANTFADAGVICTASLISPY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 REDEPACRALLPHSNFIEVFIDLFLKICEARDPKSLYKLARIKGFIKGIDDPYEPPIN 309
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LIA X. Road S. MORDALES S.D. SERR. P. BERLID M. II. TOON C.D.,

LIA X. Road S. MORDALES S.D. SERR. P. BERLID M. II. TOON C.D.,

LIA X. Road S. MORDALES S.D. SERR. P. BERLID M. II. TOON C.D.,

BARLI G. M. RESOR T.M. ROGHAN, C.L. SERRERE S. ROAD M. II. Y. M.

RAGIO K. S. CECHOLIN A. SERR. M. L. BEL G. VER AND S. BERLION L. S. SERRER S. BERLION C.S. SERRER S. BERLION C.S. SERVER S. BERLION C. S. SERVER S. SERVER S. S. SERVER S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wire Yook (Re.) 2, created)
19-09Y-2000 (Rel.) 19, created)
19-09Y-2000 (Rel.) 19, tests sequence update)
19-09Y-2001 (Rel.) 10, tests sequence update)
19-09Y-2011 (Rel.) 10, tests 1, tests 2, tests 2,
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                                                                            34: Indels
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            Pred. No. 5.5e-55;
72.9%; Pred. mc.
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                                                                            Matches 156: Conservative
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            Best Local Similarity
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Mrw-2000 (Rei. 39, Last espence update)
16.027-201 (Rei. 40, Last amorbation update)
17.027-201 (Rei. 40, Last amorbation update)
18.027-201 (Rei. 40, Last amorbation update)
18.027-201 (Rei. 40, Last amorbation update)
18.027-201 (Rei. 40, Leise) (Agradenosine-7-phosphosulfate 31.
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Pred. No. 6.7e-51;
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Pram. Proposis pred kinase.
Proposi: PROSISS; ARE kinase; 1.
Proposi: PROSISS; ARE kinase; 1.
Proposi: PROSISS; ARE kinase; 1.
Proposivoviation; transit peptide; Ghloropjaet.
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ADENYLYLSULFATE KINASE 2.
ATP (POTENTIAL).
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-!- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STMILADITY
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NCBI_TaxID-1423;
                                                                                                                                                                                                        Mendel; 28076; Arath;1772;28076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 CPSPKAMAKOVICYLEENGYLO 342
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                                                                                                    EMBL; AF043351; AAC39520.1; -.
                                                                                                                                     EMBL; AL035708; CAB38907.1; -. EMBL; AL161596; CAB80657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 AA; 31977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.6%;
Best Local Similarity 71.8%;
Matches 145; Conservative 20
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      STATEMENT
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- PATHMAY: SECOND STEP IN THE SULFATE ACTIVATION PATHMAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE BIOSNATHESTE PATHMAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.

    -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
    -!- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.

                                                                                                                                                                                                                                                                     In) Plant Gene Register PGR98-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402:769-777(1999)
                                                                                                                                                                                                                                                                                                                                                                         COLIMBIA:
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
CBI TaxID+3702;
                                                                                                                                                                                                                                          Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV.
                                 $\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\fra
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or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                PORMS THE PHOSPHOSERINE INTERMEDIATE (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 IRHGLNAGLGFSEEDRKENIRRIGEVAKLFVDAGVVTSTAFISPFREDRDNVRGILDDGE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 PIEVFIDLPLAICEBARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIKMKDEECPSP 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphotransferase).
Penicillium chryogogamu.
Buktryota: Pungi. Ascomycota; Euzizomycotina; Eurotiomycetes;
Buctryota: Prichocomaceae; mitosporic Trichocomaceae; Penicillium
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-: SIMILATITY: BELONGS TO THE APS KINASE PAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.3%; Score 534.5; DB 1; Length 202; 53.8%; Pred, No. 4.8e-33;
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70-MX-2000 (Rel. 39, Last sequence update)
70-MX-2000 (Rel. 39, Last sequence update)
70-MX-2000 (Rel. 39, Last sequence update)
70-MX-2000 (Rel. 29, Last sequence update)
70-MX-2000 (Rel. 29, Last sequence update)
70-MX-2000 (Rel. 29, Last sequence update)
70-MX-2000 (Rel. 20, Last sequence upd
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-- FUNCTION: CARLYZES THE SYNTHESIS OF ACTIVATED SULFATE.
-- CARALYTIC ACTIVITY: ATP + ademylylsuifate = ADP + 3'-phosphoademylylsuifate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 53.8%; Pred No. 4.8e-33;
Matches 106; Conservative 28; Mismatches 58; Indels
                                                                                                                                Interpor, 1PR002891; APS_Kinase.
Prican; PP01583; APS_Kinase; 1.
Prodom; P0015350; APS_Kinase; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                 6BR294F9242F1FCD CRC64:
                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY)
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InterPro; IRR002891; APS_Kinase.
Pfam; PF01583; APS_Kinase; 1.
Probon: PD002350; APS_Kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 202 AA; 22658 MW;
                                                                                                      EMBL: AP001512; BAB05208.1; -.
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012657;
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ACT_SITE
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      use by moor-profit institutions as long as its content is in no way mostlided and this statement is not removed. Usage by and for commercial entities requires a literans agreement (see http://www.isb-sib.ch/announce/or entities agreement is the commercial or entities agreement and and it to literanselsbistich).
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16-CGT-2001 (Rel. 40, Last morbalion update)
17-Cobbio ademylylaulfate kinase (DC 2.7.1.25) (APS kinase) (Ademosine-
Probpiocransferase),
Prophyspiocransferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 NITHHPAAISKSDROSLNGHKSCVLHFTGLSGSGKSVLANAVDEKLYRKGIOSYVLDGDN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Actis Res 28:437-437(2000).

- PUNCTION. CAPALYZES THE SYMTHESTS OF ACTIVATES SULFAYE.

- CAPALYTIC ACTIVITY; ATP + ademylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takami H., Nakasone K., Takki Y., Meeno G., Sasaki R., Masul N., Porji R., Hrama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 FIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 PPELYVKCPLHVCEORDPKGLYKKARNGRIKHFTGIDSPYEAPLSPDFIIE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels
                                                                                                                                                                                                                                                                                          90EC37FE4B02A123 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.4%; Score 555; DB 1;
58.5%; Pred. No. 1.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STMILARITY
                                                                                                                                                                EMBL; Y09476; CAA70655.1; ALT_INIT. 
EMBL; Z99109; CAB12931.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
                                                                                                                                                                                                                                Subtilist; BG13105; yisz.
InterPro; IPR002891; APS_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 AA; 22304 NW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOSYNTHETIC PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYC1_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYC1_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114449888888888
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          entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liécèrio (par. que ceretal)

16-cerio (par. que ceretal)

16-cerio (par. que mar amenda que que de la ceretal de l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 GDNVRHGLNRDLGFTEADRVENIRRVAEVAKLMADAGLIVLVSFISPFRGERRMARELME 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 BGEPIELFVOTPLEECARRDKALYEKALAGKIANPTGVSSPYBAPBSPELHKTVEED- 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 KSTNILWHNCLIGOSDROKLLGOKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 GDNLRHGINRDLSFKAEDRAENIRBVGRVAKLFADAGVICIASLISPYRBDROGRALLP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 HSNPIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIKMKDEEC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpoon A. G. Reinbridge F.C. Articles P. Abres F.A. Acensic O. K.,
Abbresses R. Abbres L.H.G. Abbres 2. Ber B. G. Ber Ber G. S.
Berde R. F. Camagod A. Camagod E. B. Bar G. S. Ber Ber G. S.
Berde R. F. Camagod C. A. Camagod E. R. A. Carres C. M. Carrer R.
Ochator M. C. Oldsho C. Core F. F. Costa R. R.C.R. Costa Refer C. P.
Perinson M. P. Perinson A. S. Bertson V. Camagod R.C.R. Costa Refer O. M.
Francis J. S. Franco S. C. Franco N.C. Fromm M. Frankan L. A.
                                                                                                                                                                                                    3.
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Bacteria: Proteobacteria: gamma subdivision: Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.5%; Score 502.5; DB 1; Length 633;
49.7%; Pred. No. 4.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  696BCA683D4B3111 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633 AA; 69279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 PSPKAMAKQVLCYLEEN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 -- PVALALKIEAFLDRH 629
                                                                                                                                                           EMBL: II59507: AAB95249.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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STRAIN=9A5C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
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09PD78;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             We will Dissolve Dr. T. Descapation in the Constant of March Dr. Constant M. Werrent D. Stock C., Hellings N., Americanour T., Coolseek E., Verrent D. Stock C., Hellings N., Americanour T., Coolseek E., Verrent D. Stock C., Hellings N., Americanour T., Coolseek E., Verrent D. Stock C., Hellings N., Americanour D. Stock C., March D. Stock 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 STNILMHNCLIGOSDBOKLIGOKGCVVWITGLSGSGKSTLACALSREL--HCRGHLTTVL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DGDNIRFGLNKDLGFSEADRNENIRRIAEVAKLFADSNSIAITSFISPYRKDRDTAROLH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-662-236 (Ra. 77. Last sequence update)
15-662-236 (Ra. 77. Last sequence update)
15-627-236 (Ra. 77. Last seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHYSTOLIA ASSOCIATED (POTENTAL).

SIMILARIY: IN THE N-TERMINAL SECTION, BELONGS TO THE GTP-HINDING ELLOWENTY IN THE N-TERMINAL SECTION, BELONGS TO THE GTP-HINDING TRAILLY CHEWNROD SHEWRILLY. STRAILBATTY: IN THE C-TERMINAL SECTION; BELONGS TO THE ADS KINASE.
                                                                                                                                                FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 STRITFHASALTRSERTELRNORGLIMITGLSASGKSTLAVELEHOLVRDRRVH-ATRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 DGDNLRHGINRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRAL- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 ------LPHSNFIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPIN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium sp. (strain BR816).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Indels 20;
                                                                                                                                                                                                                                                                                                                                                               Length 211;
Transferase: Kinase: Cysteine biosynthesis: ATP-binding:
                                                                                                                                                                                                                                                        7DDC4BDA867FE7C2 CRC64:
                                                                                                                                                                                                                                                                                                                                                               505; DB 1;
No. 7.9e-31;
                                                                                                       ATD (DOTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 GEIVIKMKDEBCPSPKAMAKOVLCYLBENGYLOA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 PE--VHVKNYELPVQDAV-KQIIDYLDTKGYLPA 208
                                                                                                                                                                                                              STATIARITY
                                                                                                                                                                                                                                                                                                                                                     Score 505;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                        211 AA; 23770 MW;
                                                                                                                                                                                                                                                                                                                                                               51.48;
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 51.49
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                              Phosphorylation.
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007309:
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ACT_SITE
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This SMISS prof metry is opergight. It is produced through a collaboration between the Seiss institute of institutes of institutes of the set of the Seiss institute. There are no restrictions on its the European and institutes "there are no restrictions on its medited and this statement is not removed. Using the Seiss in the set of the statement is not removed. Using the Seiss in the Seiss in
SULFURIASE ACTIVITY (BY SIMILARITY).
--- FUNCTION: ARS KINASE CATALYZES THE SYMTHESIS OF ACTIVATED SULFATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: FIRST AND SECOND STEES IN THE SULFATE ACTIVATION PATHWAY. FIRST REACTIONS OCCURE SEALY IN THE REDUCTIVE BRANCH OF THE TREENE BLOSYNHETIC PATHWAY.
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- EINCHATION PROFOR FAMIL: SECTION; BELONGS TO THE APS KINASE
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CTP (BY SIMILARITY).
CTP (PY SIMILARITY).
ATP (POTRITIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: ATP SULFURIDASE MAY BE THE GIPASE, REGULATING ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cysteine blosynthesis; Transferase; Nucleotidyltransferase; GTP-binding; Kinase; ATP-binding; Multifunctional enzyme;
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43.9%; Pred. No. 8.5e-30;
Live 42; Mismatches 76;
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InterPro; IPR002891; APS_Kinase.
InterPro; IPR000475; GPP_EETO.
ThterPro; IPR0004161; GPP_EFTU.
Pfam; PF01583; APS_Kinase; 1.
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PRIME: PR00315; ELONGATHECT.
ProDcm; PD002350; ASS_Kinase; 1.
PROSITE; PS00301; EFACTOR_GTP: 1
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This SINES-SEAT entry is opergright. It is produced through a collaboration between the Suisa institute of Sinifornamities and the DBMs obstration here proper a collision small smalltitue. There are no extractions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial smalltimes all comes a spreament (see http://www.isab-sin.ch/announce) antities equitee a license apresent (see http://www.isab-sin.ch/announce).
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Occ. 196 (Rel. 14, Loss medium)

Many 100-196 (Rel
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SILLEWRIAGES ACTIVITY (BY SIMILARITY).

--- FUNCTION ARE SIMILARIZED THE SYNTHESIS OF ACTIVATED SULEWIE

--- BUSINIANITY).
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400 NRVLGSFILIDRHSNATVGAG-----TLDSGVHRASNVHWQPLDIDHVARARIKGGT 451
                                                                                                                                               226 RVGBVAKLFADAGVICIASLISPYRRDRDACRALLPHSNFIBVFIDLPLKICEARDPKGL 285
                                                                                                                                                                                                                                                                                                                                                       GCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLDGDNLRHGLNRDLSFKAEDRAENIR
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Rhizobiaceae; Rhizobium.
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Vanderleyde J., Marthez Romero E.,
Tigolation and characterization of Rhizoblum tropici Nod factor
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Mol. Plant Microbe Interact. 9:492-500(1996).
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KINDSE ACTIVITY, MITCH MEDATES THE STEPS IN THE SULFATE
ACTIVATION PATHENT, THE FIRST STEP IS THE TRANSFER OF A SULFATE
GROUP TO ATP TO YIELD ADDROSINE 5'-FHOSPHOSULEATE (APS), AND THE
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                                                                     MEDINE-Feel) brain;
MEDINE-Feel) Pubmed-9668121;
Venkatach4913467; Pubmed-9668121;
Venkatach491346 K.V., Akita H., Sirott C.A.;
Venkatach418m M. Sirott C.A.;
Venkat
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Standissaw K. Sakatlora K. Salkalora K. Sakatlora K. Colk cloning, appression, and charcetization of the human bifunctional ATP sulfurylasey demostra 5-posphosulfare kinase
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InterPro; IPR002650; ATP-sulfurylase.
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ProDom; PD002381; ATP-sulfurylase; 1.
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Pfam; PF01747; ATP-sulfurylase; 1.
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MIM: 603262: --
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19-1047-2007 (Rel. 14. Created
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WILL HURSTEAN CONTROLL

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"swifetion in high endothelialvenules: cloning and expression of the
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send an email to license lish-sib.ch).
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MEDLINE-98236023; PubMed-9576487;
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                                                                                                        SMBL; U47272; AAB08984.1; -.
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043252; 043841; 075332;
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1.6-CT-2000 (Rel 1, G. Lost sequence update)

1.6-CT-2000 (Rel 1, G. Lost sequence updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGKSTLACALSRELHCRGHLTYVLDGDNLRHGLNRDLSFKAEDRAENIRRVGEVAKLFA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 DAGLUCITSFISPYTQDRNNARQIHEGASLP---FFEVFVDAPLHVCEQRDVKGLYKKAR 178
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Li H., Deyrup A., Mensch J.R. Jr., Domowicz M., Konstantinidis A.K.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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N. P. INTERESSES ACTIVITY.
R. A. INGESSES OF ACTIVITY.
R. A. I. A.
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Pred. No. 1.5e-29;
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                                                                                                                                                                                                 SHLFATE ADENYLYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                PP-MOTIF (BY SIMILARITY)
                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue-Brain;
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ACT_SITE
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PPSI_MOUSE
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.. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE -i - SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE OF PROTEINS, CARBOHYDRATES, LIPIDS, DRUGS AND XENOBIOTICS. CARTILAGE

This STRISS EXPORT entry is deepyright. It is produced through a colliboration between the Savis institute of Holoforastics and the SBHs outstation. The Burgopan aboutcometic and the SBHs outstation was by non-profit institutions as long as its operating and its week by non-profit institutions as long as its operating to the second and the second an ATP (POTENTIAL). FORMS THE PHOSPHOSERINE INTERMEDIATE (BY Transferase: Nucleotidyltransferase; Kinase; Multifunctional enzyme: ATP-binding; Multigene family ADENYLYLGUIENTE KINASE. 1 7220 ADENYLYLGUIENTE KINASE. ADENYLYLSULFATE KINASE. SULFATE ADENYLYLTRANSFERASE. SIMILARITY). InderPor, IRRO02891, APS\_Khnase.
InderPor, IRRO02801, APS\_khnase.
Pfam, PR01363, APS\_khnase; I.
Probom, PD002550, APS\_khnase; I.
Probom, PD002550, APS\_khnase; I.
Probom, PD002550, APS\_khnase; I.
Probom, PD002550, APS\_khnase; I. EMBL; U34883; AAC52328.1; -. MGD; MGI:1330587; Papss1. NP\_BIND ACT\_SITE

60; Indels 26; 27.1%; Score 495; DB 1; Length 624; 46.1%; Pred. No. 1.5e-29; 38; Mismatches Conservative Similarity Ma. Local S... 106; Query Match

B487EFAF9B78BE3E CRC64;

PP-MOTIF

624 AA; 70794 MM;

125 EAPHSPVKEKPVMSN----IGKSTNILWHNCLIGQSDRQKLLGQ----KGCVVWITGLS 175 Gaps

9

36 DAGVICIASLISPYRRDRDACR----ALLPHSNFIEVFIDLPLKICEARDPKGLYKLAR 290 I22 DAGLUCITSFISPYTODRNNAROIHEGASLP---PPEVPUDAPLHUCEORDUKGLYKKAR 178

291 TCKIKGFTGIDDPYEPPINGEIVIKMKD---EECPSPKAMAKOVLCYLEE 337 179 AGEIKGFTGIDSEYEKPEAPELVLKTDSCDVNDC-----VQQVVELLOE

215 AA

STANDARD:

CYSC OR VC2558.

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noboy)throaterase sentint | (R. 27, 74) (Statler deboylate choice anonferace) (27, 71, 27) (Statler deboylate choice anonferace) (ATP selfort) the litter and statler and stat
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-- I-SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GIP-BINDING BLOMGATION PACTOR PARILY. CYSNIVODO SUBFABILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE-92288403: PubMed-2520820;
WHEDLINE-92288403: PubMed-2520820;
Whicheofiel sequence and protein products of two new modulation genes
Two-flootide sequence and protein products of two new modulation genes
Whichely Mailtoit, node and node;
William Microbe Interact. 2:181-194(188).
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Personerer C.,
The Rhizoblum mellioti host range nod0 gene encodes a protein which
the shares backlogy with franshaton elongation and initiation factors.";
Nol. Microbiol. 3745-785(1989).
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-:- SUBUNIT: SULFATE-ACTIVATING ENZYMES, NODP AND NODQ, MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpor, IPR0002891; APS_Kinase, Interpor, IPR000795; CPL_ERTU, Interpor, IPR0004761; CPL_ERTU_D2. Pfam; PP001893; APS_KINASe; II. Pfam; PP001993; CPL_ERTU; I. Pfam; PP03144; GPP_ERTU_D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-RCR2011 / SU47;
MEDLINE-89313304; Pubmed-2546009;
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EMBL, M68858; AAA26343.1; -.
EMBL, AE007237; AAK65127.1;
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InterPro; IPR00289
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SEQUENCE FROM N.A.
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STRAIN-1021;
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                                 This SINES POUR entry is copyright, it is produced through a collaboration between the Suss institute of Bioliformatics and the Biblio outsetton. The Barpoon and individual mutitude where two nettitions on its use Promotorial institutions as long as its content of an one profit institutions as long as its content of an entities entry and a series a license agreement (see http://www.isb-iib.ch/mnnonce/or send an easil to licenseisb-iib.ch/mnnonce/or send an easil to licenseisb-iib.ch/mnnonce/
                                                                                                                                                                                                                            MELLING-19983) Publication of the Author Recognition Relations and an analysis of the Author Recognition Relation Relations and the Relation Relations and the Relation Relations and the Relation Relations and the Relations and t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 GDNVRHGLCSDLGFSEQDRRENIRRIGELAKLMSDAGLIVLTARISPHRAEROMVRDLLP 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13, Last sequence update)
41, Last anotation update)
42, Last anotation update)
70 (Includes: Sulfate
                                 Proteobacteria; gamma subdivision; Vibrionaceae: Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphoadenylylsuifate.
-- PATHWAY: SECONO STEP IN THE SULFATE ACTIVATION PATHWAY. THIS SEARCY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.1%; Score 494.5; DB 1; Length 215; 48.3%; Pred. No. 4.8e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Universet 46:477-483(2000).
- PUNCT 406:477-483(2001).
- CARALTIC ACTVITY: ATP + adentiface = ADP + 3'-
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ProDom: P0002350; ARS_kinase; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 AA: 23906 NW: 83B9EE2F295CDDF6 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHETIC PATHWAY.

-!- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
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                                                                                                                                                                                                  / SEROTYPE 01;
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73444;
01-73442;
01-734-1990 (Rel. 13, Created)
01-MAR-2002 (Rel. 41, Last sequent
01-MAR-2002 (Rel. 41, Last ennotes
NodQ bifunctional enzyme (Nod1ata)
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OF PROTEINS, CARBOHYDRATES, LIPIDS, DRUGS AND XENOBIOTICS. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
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                                                                                                                                                                                              --- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULPATE ADENYLYLTRANSFERASE FAMILY
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3.6e-29;
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Aspeptillus nichlans."; BMBL/GenBank/DDBJ databases.
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525 PP-MOTIF (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PARIMANT THE PLEATE THE OFFERS IN THE SILENTER CATAVATION PARIMANT THE PLEAT STEP IS THE PRANSERS OF A SILENTER CATAVATION PARIMANT THE PLEAT STEP IS THE PRANSERS OF A SILENTER PLAN ADMINISTRY (ASS), AND THE PRANSERS OF A SILENTER PROPERTY O
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L-SELECTIN LIGANDS IN ENDOTHELIAL CELLS (BY SIMILARITY).
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- CMTATIC SCIVITY: AP + adenylylsulfate - ADP + 3'-

phosphosphosdenylylsulfate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 RADNVHWHALEVNKSARSAMKNQLPAVLWFTGLSGSGKSTIANELDRILHAQGKHTYLLD 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496 GDNVRHGLNRDLGFTEEDRVENIRRVAEVAKLMADAGLIVLVSFISPFRDERRMARELME 555
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Submitted (AKY1997) to the EMBL/GenBank/DBJ databases.
I- FDWL710N: BIPINKTIONAL BRIZHE WITH BOTH ATP SULPURIASE AND APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea Pig).
Medrarycia, Metazoa, Chorada, Craniata; Vertebrata; Euteleostomi;
Memmalia; Euthoriaza Rodentia; Hystricognathi; Cavidae; Cavia.
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GTP (BY SIMILARITY)
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ACT_SITE
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PPS1 CAVPO

3

Gaps

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This SNISS-FROM entry is copyright. It is produced through a collaboration between the absis institute of insidenties and the DBML outstation. The European Bioinformatics institute. There are no restrictions on list only now by months profit institutions as long as its concent is in no way expensive proportion in the proportion of the
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                                                                                    phosphoadenly is suifate
- PATHANT SCOOD STEP THE SULFACE ASSIMILATION PATHAN THAT
LANG TO THE BIOKYPHIESTS OF WETHINNING FAMILY.
- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
-i- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: F08866; CAA70089.1;
fincePro: TPR00289; AMS_Kinase.
FPGMS: PF01589; AMS_Kinase. 1.
FPGMS: FP01589; AMS_Kinase. 2.
FPGMS: Kinase: Cycleine biosynthesis, AFP-binding;
FFANSEcrase; Kinase; Cycleine biosynthesis, AFP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA; 23028 NW; 6AADD483E2BCA1CD CRC64;
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NP_BIND 31
ACT_SITE 105
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143 STNILWHNCLIGGSDROKILGOKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLDG 202 61; Indels 12; Gaps Ouery Match 26.64; Score 486; DB 1; Length 206; Best Local Similarity 50.74; Pred. No. 28-29. No. 28-29. Indels 3 106; Conservative 30; Mismatches 61; Indels 3

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61 DNVRFGLNKDLGFSDADRNENIRRIAEVAKLFADSSSIAITSFISPFRADRDTARKLHEV 120 2 ATNIT-HHAGLTRNERNOLRKOKGLITWLTGLSASGKSTIAVELEHOLLORGLHAYRLDG 60 203 DNLRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRAL--L 260 à a ò qq

261 PHSN-----FIEVFIDLPLKICEARDPKGLYKLARIGKIKGFTGIDDPYEPPINGEIVI 314

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121 PTPNDSTGLPFVEVFVDVPIEVAEKRDPKGLYKKARRGIIKEFTGISSPYEAPENPEVHV 180 315 KMKDEECPSPKAMAKQVLCYLEENGYLQA 343 181 KNVD--LPIQEAV-KQIIDYLDSKKLLDA 206 g

Search completed: November 2, 2002, 01:52:18 Job time : 22 secs

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1 RPFHFINQTEPLYTHTQQPP.....PKAMAKQVLCYLEENGYLQA 343
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562222 seqs, 172994929 residues Gapop 10.0 , Gapext 0.5 Searched:

BLOSUM62

Scoring table:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Sparcha; Spacteria: Sphudi: Sphuman: Sphuman: Spho: Spho: Space: Space: SPTREMBL 19:\* Database :

sp\_vertebrate:\* sp\_unclassified:\* sp\_rvirus:\* sp\_bacteriap:\* sp archeap:\* 116333333

sp\_plant:\* sp\_virus:\* Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIPE

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OCT THE PARTY OF		g	09SRW7	09SE92	09FJX1	09SQR9	Q97MT8	99NDP8	081351	092VH6	090XY2	09A882	022501	093HS6	09P7G9	09EYY1	027128	Q9UE98
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18	495	27.1	624	-	096TP4	1 homo
13	489.5	26.8	603	4	Q96FB1	ОшО
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77	482	26.4	614	4	Q9up30	homo sa
22		26.4	614	4	Q9BZL2	homo
23	482	26.4	614	*	950460	homo
24	482	26.4	619	47	09UHM1	Omo
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28	475	26.0	202	3	09C2Y6	Q9c2y6 saccharomyc
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31	433.5	23.7	211	~	Q9R6K6	
32	333	18.2	553	2	093N43	
33	308.5	16.9	178	7	09ADG4	
34	302.5	16.6	574	3	096005	
35	246.5	13.5	581	3	Q96UP1	Q96upl cryptococcu
36	179	9.6	170	16	Q9PMP2	
33	150.5	8.2	160	2	09X5T9	Q9x5t9 streptomyce
38	120	9.9	361	4	096059	
33	117	6.4	361	4	09н8G2	
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41	111.5	6.1	396	7	Q9X922	Q9x922 streptomyce
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ALIGNMENTS

208 AA

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137 MSNIGKSTNILWHNCLIGQSDRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCRGHL 196 Gaps 45.7%; Score 834; DB 10; Length 208; 74.8%; Pred. No. 5.5e-61; tive 28; Mismatches 24; Indels 0; Best Local Similarity 74.89 Matches 154; Conservative Query Match à

2BA510DC0F35EA33 CRC64;

SEQUENCE 208 AA; 23146 MW;

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197 TYVLOGDNERHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICLASLISPYRRDROG 256 1 STYGNSTNIFWQESPIGKTERQKLLNQKGCVVWITGLSGSGKSTLACSLSRELNNRGKL 60 a õ

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PASARYOCA: VITIGIDANTON: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Majoollophyta; Aspectophyta; Majoollophyta; Majoollophyta; eudicoty; edons; core eudicots; Rogidae; eurosida II; Erassicales; Brassicaceee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GKSTNILWHNCLIGGSDRQKLLGGKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 DGDNLRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRALL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 DGDWVRHGLNSDLSFEADDRAENTRRVGEVAKLFADSGLICLASLISPYRIERAACRALL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 PHSNFIEVPIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIKMKDEE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsia thalian (Nouse-ear cress).
Spermatophyta: Tracheophyta: Spermatophyta: Tracheophyta: Spermatophyta: Mystidiplantes; Streptophyta: Spermatophyta: Mystidiplantes; Streptophyta: Ospermatophyta: Mystidiophyta: Hostidicoyladens; Core editoris; Rosidae; Spermatophyta: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAINERY COLOMBIA.

STRAINERY COLOMBIA.

TAT. KRUIS, T. YOU C.D. BERITON M., CREADY T. H., Hasse B.,

Bounding C.M., KON C.D., CAV., Uterahoek T.B.,

Broanding C.M., Marrian M.C., Fribard C.M.,

Branding C.M., Marrian M.C., Fribard C.M.

Branding C.M., Marrian M.C., Fribard C.M.

Branding C.M., Marrian M.C., Fribard C.M.

Branding C.M., Strainer M. Strainer,

Branding C.M., Strainer,

Branding C.M., Strainer,

Proceen PROPERTY AREA Marses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Territoria analysis of Arabicosis thilasa chromosome 5. VI. Sequence features of the regions of 1.57.185 pp covered by 19 Mark 12, 50.785 of 19 Mark 12, 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 290:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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01-MAY-2000 (TERMBLEEL 13, Last sequence update)
01-MEC-2001 (TERMBLEEL 19, Last annotation update)
PUTATIVE ADBWILTGLUENTE KINASE, 3' PARTIAL (PRAGNERT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 290 AA; 32195 MW; BB7FB12990A6F6P8 CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADBNILYISJURARE-LIKE PROFEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.3%; Score 755; DB 10;
69.8%; Pred. No. 2.7e-54;
tive 28; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 AA
                                                                                                                                                                                                                        Arabidopsis thallana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-COLUMBIA;
MEDLINE-98403884; Pubmed-9734815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 CPSPKAMAKOVLCYLEENGYLO 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 SSECEMADIVVSYLDONGYLK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            datches 141; Conservative
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Rakryota Vitálplantae: Streptophyta; Babryophyta; Trachasphyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade;
Spermatophyta; Mandopoaneae; Zea.
W.H.I.Taxifa-477;
                                                                                                                                                                    121 REMIONSSFIEVFNAMSLOLCEARDPKGLYKLARACKIKGFIGIDDPYRSPLNCEIELKE 180
61 SYILDGDNLRHGLNKDLGFKAEDRVENIRRVGEVAKLFADAGLICIASLISPYRKDRDAC 120
                                                                                                      257 RALLPHSNFIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIKM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 EGEGRGARTHCHRGIGRWVRRRRRNG-----AAPGEAPHSPVKEK--PVMSNIGK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 STNIEWHNCLIGGSDRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLDG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 SSNIFWHDCPVGKIDRQNVLKQKGCVVWITGLSGSGKSTLACTLGRELHTRGKLAYVLDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 DNIRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRALLPH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 DNLRHGLANDLGFRAEDRAENIRRV--VAKLFADAGLVCIASLISPHRIDESSCRALLSD 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 ONEGD -----RREKLRGTPLVECTGDRSVEEQPEHAGVEGKAWKMSSTVPK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 SSFIEVFLNMSLELCEARDPKGLYKLARAGKIKGFTGIDDPYEAPLNCEIEIKEVDGVCP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 PIPILAVILVN----PQRAPPVLPGLTPSDAPLPALVIHGLIPRSSHSSAGLASDSGRR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BERTAIN-O' BEACH MITZ; CHEMBLIO S. 12 TO BEACH MITZ CHEMBLIO S. 12 TO BEACH MITZ CHEMBLIO S. 12 TO BEACH MITZ CHEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.5%; Score 812.5; DB 10; Length 288;
53.9%; Pred. No. 4.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TFBMELrel. 13, Created)
MAY-2000 (TFBMELrel. 13, Last sequence update)
01-JUN-2001 (TFBMELREl. 17, Last annotation update)
ADENOSINE-5'-PHOSPHOSULENTE KINSE (EC 2.7.1.25) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 AA.
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                                                                                                                                                                                                                                                                                                          317 KDEBCPSPKAMAKQVLCYLEBNGYLO 342
                                                                                                                                                                                                                                                                                                                                                                                                                 181 KEGECPSPVAMAEEVISTLEDKGFLQ 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 172; Conservative
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Q9FJX1;
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"Colmaractivatarian on Enachyury downstream notochord genes in the Ciona intestinalis emergo." Askarion or De Besin/Censan/Dubb databases. Submitted (2.78-2000) to the Besin/Censan/Dubb databases. Besin/Censan/Sin Responsible 1.8 kickase. Interepro; 1800/881, ARC Sulfurylase.
                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Phlebobranchia,
Clonidae, Clona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOTTA K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y., Satoh N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GKSTLACALSRELHCRGHLTYVLDGDNLRHGLNRDLSFKAEDRAENIRRYGEVAKLFADA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 APGEAPH-SPVKEKPVMSNIGKSTNILWHNCLIGOSDROKLLGO----KGCVVWITGLSGS 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ASATANHGDDIQEKPPM----SSNIVYQQHHVSRDERGQVMGKGAFRGCTVWFTGLSGA 56
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GLORO Y., LEMSTER T.;

"Cloning of the CoRM for 5'-ademylyisulfate (APS) kinase from the marine macroalga Enterconcepha Intestinalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51: Indels 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 30.8%; Score 563; DB 5; Length 618;
Local Similarity 54.5%; Pred. No. 4.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (UNN-1999) to the EMBL/GenBank/DDBJ databases
EMBL: ANG 1992; ANG 20865 L.I.
InterFor: IPRO/2891, APS. Kinae.
From: PPO/1891; APS. Kinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 618 AA; 69559 MW; 75223CCB022BC297 CRC64;
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10.100'-1998 (TERMILE) 08, Last sequence update)
10.100'-2001 (TERMILE) 19, Last annotation update)
10.100'-2001 (TERMILE) (TERMILE)
10.100'-2001 (TERMILE)
                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-50T-2001 (TrEMBLrel. 17, Last senotation update)
APP SULFURFLASE, APP KINNE.
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                                                              618 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 GFTGIDDPYEPPINGEIVIKMKD---EBC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF01583; APS_kinase: 1.
Pfam: PF01747; ATP-sulfurylase: 1.
ProDom: PD002359; APS_kinase: 1.
ProDom: PD002381; ATP-sulfurylase: 1.
                                                              PRT:
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Ciona intestinalis.
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                                                                                                                                                                                                                                                                                                                                                                 137 MSNIGKSTNILWHNCLIGGSDRQKLLGGKGCVVWITGLSGSGKSTLACALSRELHCRGHL 196
                                                                                                                                                                                                                                                                                139 NIGKSTNILWHNCLIGOSDROKLIGOKGCVVWITGLSGSGKSTLACALSRELHCRGHLTY 198
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Clostridium.
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                                                                                                                     34.6%; Score 632; DB 10; Length 152; 77.0%; Pred. No. 1.5e-44;
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                                                                                                                                                                                   15: Indels
                                                       152 AA: 16974 NW; DBAC812B71D50DE5 CRC64;
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Last annotation update)
                                                                                                                                                                                   20: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 RALLPHSNFIEVFIDLPLKICEARDPKGLYKL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 REMIONSSFIEVENINGLOLCEARPHYSIC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2001 (TrEMBLrel, 18, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE007523; AAK78088.1; -.
InterPro; IPR002891; APS_kinase.
Pfam; PF01583; APS_kinase; 1.
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Kinase; Complete protecome.
SEQUENCE 200 AA; 23001 NW: FF
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01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                   Matches 117; Conservative
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134 KPVMSNIGKSTNILWHNCLIGQSDRQKILGQ----KGCVVWITGLSGSGKSTLACALSRE 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KKLCINLERSINVYXOAHHVSRSKRBOIVGIRGERGCIIWIJGLSGAGKTIISFALERY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FOR NA.

MEDIANCE 19189 / CB15.

MEDIANCE 191899 / CB15.

MEDIANCE 191899 / CB15.

Elsen I. T., Relichburg T. V., Labb M. T., Panisen I. T., Relson K. E., Elsen I. T., Relichburg T. V., Labb M. T., Chab M. M. Anddeck I. B. D. Alley M. M. Chab M. C., Phales D. P. D. Elsen I. T., Delkon K. T., Delkon M. C., Panise C., Phales N. D., Ely B., Delkon M. C., Delkin M. M. Shelphus C., Phales N. D., Ely B., Cholony J. T., Delkon M. M. S., Pollin M. E., Shelphus C., Phales M. M. S., Repulson C., Phales M. M. P. Derry K., M. Cholony J. S., Salt J., Craven M. B., Khour H., Shelty J., Berry K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paga rubripes (Japanese pufferfish) (Takituy rubripes),
Artyota, Wetaona Chordana (Zaniata; Wetdanata; Butelaoatomi,
Artinoparyyli; Weoperyyli; Teleostel; Butelaostel; Meocleostel;
Artinoparyyli; Meoperyyli; Percomorpha; Tetraodontilozmes;
Tetraodontide; Takituyu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Conserved Synteny between the Fugu and human FTBN locus and the evolutionary conservation of vertebrade PTBN function."; oncopene 2015594-7561(201).
BREIL NESSSESSEN ALOUGH ST. 1. SESSIL48377C4169 CRC64; SEQUENCE 613 Ap. 65948 WH: 28ES0148377C4169 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
MEDIJNB-21455682: PubMed=11571655;
Yu W.P. Pallen C.J., Tay A., Jirkk P.R., Brenner S., Tan Y.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-07NY-2001 (TERBILEG. 17), Created)
01-07NY-2001 (TERBILEG. 17), Last sequence update)
01-07NY-2001 (TERBILEG. 13), Last emototion update)
SULANT DERVIATE DANSFERASE, SUBUNIT 1/ADENILIZER KINSE.
071437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caulobacter crescentus.
Bacteria: Proteobacteria: alpha subdivision: Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3 **PHOSHHOADEWOSINE 5 **PHOSPHOSULATE SYMTHASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 PPINGELVIKMKD---EECPSPKAMAKQVLCYLEENGYL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 SPDRPDLVLKTGELTVDEC-----LOQVLELLRENDIL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.9%; Score 509.5;
47.9%; Pred. No. 1.1
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                                                                                                                                                                                                            322 PSPKAMA 328
                                                                                                                                                                                                                                                                              615 PTDTATA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venkatesh B.;
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Q9A882
       us-09-720-384a-4.rspt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 RCIGRWYRRRRNGAAPGEAPHSPVKEKPVMS--NIGKSTNILWHNCLIGQSDRQKLLGQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 KGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLDGDWLRHGLNRDLSFKAEDRAEN- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 IRRVGEVAKLFADAGVIC----IASL----ISPYRRDRACRALEPHSNFIEVFIDLP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 PHRRSEQA-----CCRRWRPPLRELHIRPIAPTRPVRERCA----GDFVECYMKIP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 LKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIKMKDE--ECPSPKAMAKQV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 IELCEGROPKGLYKKARAGLMKGFTGIDDPYEEPLEPELTITVREEGSDMNSPEAMAKQI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 RADIVHWHALEVUKSARSAMKNOLPAVLWFTGLSGSGKSTIANELDRILHAOGKHTYLLD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WELLINGSOR, PROMED-LISESURE, THEORY-LISESURE, THE STRONG THE WELLINGS THE STRONG THE WEST OF THE STRONG THE ST
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RAIAORARGSALOCAAPGTEWASCVRGSSGFTAYDVGESTNIKWHETMYSRGDKERLLNO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria alpha subdivision; Rhizobiaceae group;
Rhizoblaceae, Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                            28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.0%; Score 511.5; DB 16; Length 633;
54.0%; Pred. No. 8e-34;
                                                                                                                                                                                                                                                                                                           28.7%; Score 524; DB 10; Length 271; 44.2%; Pred. No. 2.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.10FC.2001 (TERBILGE, 1) 9. CERREGACIO

0.10FC.2001 (TERBILGE, 19). Last sequence update)

0.10FC.2001 (TERBILGE, 19). Last sequence update)

0.10FC.2001 (TERBILGE, 19). Last sentoetton update)

RIANSE PROFIETE (E. 7.7, 1.25).

MILADSHUM mediloti (Sinoritzeblum mediloti).
                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                         D9419E11BB58C052 CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                            45; Mismatches
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4 12:27:05 2002
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                                                                                                                                                                                                                                                                                                                                                                                    datches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 LCYLEENGYLO 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 FDYLEAKGFLK 240
                                                                                                                                                                                                     Transferase.
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                                                                                                                                                                                                                                         271 AN;
                                                                                                                                                                                                                                                                                                                                                       vitaritarity
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SEQUENCE 633 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim:
Matches 101;
                                                                                                                                                                                                     Kinase; T.
Mon Nov
                                                                                                                                                                                                                                                                                                                   Query Match
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70 TISPALERTLAKIGIPCYGLDGDNIRHGLCKNLGFSKEDRQENIRRVAEVAKLFADSGM 129
                                                                                                                                                                       125 EAPHSPVKEKPVMSNI-GKSTNILWHNCLIGQSDRQKLLGQ----KGCVVWITGLSGSGK 179
                                                                                                                                                                                                                                                                                                                      180 STLACALSREIHCRGHLTYVLDGDNLRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ICIASLISPYRRDRDACRALLPHSN--FIEVFIDLPEKICEARDPKGLYKLARTGKIKGF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 ICLAAFISPPOEDRLDARKIHESENVKFIEVHVSTTLEVCEORDPKOLYKKARAGOLLGF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 GDNLRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRALLP 261
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                                                                                                                                                                                                               10 EGDAMPHIKKPRYSSLSGQSTNITYQEHTISREERAAAVGRIEGFRGCTINFTGLSGAGK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 KSTNILWHNCLIGQSDRQKLLGQKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 HSNFIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIKMKDEBC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wenthing via 150 size, produced 1157318 (i. Ferre H., Minemister N. 150 size T. Okeaski S., Mitteril H., Varabil K., Eurus H., Minemister N. 150 size T. Okeaski S., Mitteril H., Varabil K., Eurus H., Chichitoxine biodynthesis A. 150 size the control of the cont
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Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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Pred. No. 3e-33;
               Length 652;
                                                                                       64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 TGIDSAYEPPENAEIILDAGKDGVQQC-----VQKVLDHLESKGLL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 TGIDDPYEPPINGEIVIKM-KD--EECPSPKAMAKQVLCYLEENGYL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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               Score 505; DB 5;
Pred. No. 2.8e-33;
                                                                                       38: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 AA.
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NCBI TaxID-29448;
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(TrEMBLrel, 19, L)
(TrEMBLrel, 19, L)
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               27.78;
                                               Best Local Similarity 48.0
Matches 109; Conservative
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Best Local Similarity
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01-DEC-2001
01-DEC-2001
               Query Match
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Q9P7G9;
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Ultrabect, T. Trank, Neelle A. Vanaheven J. Erabeleen M. White C
Salaberg S.L., Venter G.C., Shapiro L., Frase C.K.,
Fromplete general sequence of Canlaberger crescentus.',
From Maril Reads Sci. 10.S.A. 98 115-444 (2001).
From Maril Reads Sci. 10.S.A. 98 115-444 (2001).
Pagel, ANGOSZI, AAKZ1461.1; THE GTF BIRDING ELOWSKION PACFOR PARILY.
TITUS COL582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa: Nematoda: Chromadorea: Rhabditida: Rhabditoidea;
Rhabditidae: Peloderinae: Caenorhabditis.
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                                                                                                                                                                                                                                                              | InterProc | InfoOnset, ask. Instance. | InterProc | InfoOnset, ask. InfoOnset. | InfoOnset.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wild A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72987 MW; 36148F20C31AD875 CRC64;
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01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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REMILE, MESSERO CANASJORA 11 .
ILLEGENO : PRODOZDESI ANGLATINE CHERCE PROPERTIES ANGLATINE CHERCE PROPERTIES ANGLATINE CHERCE PRODUCES ANGLATINE CHERCE I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.8%;
Best Local Similarity 51.3%;
Matches 100; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 PSPKAMAKQVLCYLE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613 IDPVEARERIVANLE 627
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9

Gaps

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145 NILWHNCLIGOSDROKILGOKGCVVWITGLSGSGKSTLACALSRELHCRGHLTYVLDGDN 204
                                                                                                                                                                                                                                                                                                                                                205 LRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRALLPHSN 264
                                                                                                                                                                                                                                                                                                                                                                                                                       67 VRHGLCSDLGFSDEDRKENIRRVGEVARLMVDAGLVVLTAFISPHRAEROMVRERLGEGR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 STNILWHNCLIGGSDROKLLGO----KGCVVWITGLSGSGKSTLACALSRELHCRGHLTY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 VLDGDNLRHGLNRDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRA 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 LHEGAGLP---PFECFVDTPLDVCEQRDVKGLYKKARAGQIKGFTGIDQQYESPDAPEIQ 186
                                                                                                                                                                                                                           7 NVVWHAHPVTQQQREQHHGHRGVVLMPTGLSGSGKSTVAGALEEALHERGVSTYLLDGDN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ATNUTEOTOHYSBAKRGOVIGORGERGCTVWPTGLSGAGKTILSFALEBELVSGGIPTY 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Urechis caupo (Innkeeper worm) (Spoonworm).
Makaryota: Metazoa: Echlura: Xenopneusta: Urechidae: Urechis.
McBr. TaXID-6431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 610;
                               27.5%; Score 503; DB 2; Length 201;
57.7%; Pred. No. 9.1e-34;
tive 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 FIEVEVUTPLAICEARDEGIAKEREAGELRIFIGIDSVERAERAEI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
PAPS SYMTHETASE.
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Pred, No. 4.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 LYAGNESTIDEC ---- VOEVVSLLOKNG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT.
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MEDLINE-96096529; pubMed-8522184;
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                               Query Match
Best Local Similarity 57.7%
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 DNLRHGLARDLSFKAEDRAENIRRVGEVAKLFADAGVICIASLISPYRRDRDACRAL--- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 DNVRFGLASDLGFSEQDRIBNIRRIGHVAKLFADACVVAVTSEISPYRKDEDQAREFHKK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 -- LPHSNFIEVFIDLPLKICEARDPKGLYKLARTGKIKGFTGIDDPYEPPINGEIVIK-- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 DGLP---FIEVYVECPVEVABORDPKGLYKRARAGETGISAPYEAPISPEIVVSSH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                        wood V. Rajandream M.A., Barrell B.G., Brown S., Harris D., Submitted (FBR-2000) to the pw60/denbank/DDBJ databases. BMBL, ALISBOSE, CAMPAZA II. Therero: IPPROUSES! THE KLAINSE. FPROUSES! THE KLAINSE. FPROUSES! THE KLAINSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.6%; Score 503.5; DB 3; Length 2/
51.7%; Pred. No. 8.4e-34;
tive 29; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA; 22669 NW; A5P7E4D53D76353B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22504 NW: 6BB20A71AB03D712 CRC64;
                               spacij82.ii.
Schlizosechaarcmyces pombe (Fission yeast).
Bukaryota, Fundi. Ascomycota: Schlizosaccharomycetes;
Schlizosaccharcmycealas; Schlizosaccharomycetaceae;
Schlizosaccharomyces.
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Last annotation update)
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"Welfhoune recycling in Klebstella aerogenes.";

"Bella, Ystolesis Aedicatella, "Stolesis Aedicatella,"

Theorem 1800/881, MeS. Kinase.

Friam PROJSS1 NPS Kinase.

Probas PROJSS1 NPS Kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF01583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 TOSIEEC -----VEKIVNYLLE 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 105; Conservative
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ADENYLYLSULFATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                   NCBI_TaxID-4896;
                                                                                                                                                                                                                                                                                                                                         STRAIN-972H-;
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Gaps

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on:

November 2, 2002, 01:52:23 ; Search time 2249 Seconds (Withfout alignments) 3191.553 Million cell updates/sec

US-09-720-384A-4
1856PPINGTEDLYTHTQOPP......PRAMAKOVICYLEBNGYLQA 343 RLOSTIM62 Perfect score: Scoring table: Sequence: Title

Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0

3595312 1797656 seqs, 10463268293 residues Total number of hits satisfying chosen parameters:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

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## ALIGNMENTS

RESULT 1 AF044285 LOCUS

AF044285 1086 bp mRNA linear PLM 11-AUG-1998 Catharanthus roseus adenosine-5'-phosphosulfate-Kinase (CRakh) mRNA, complete cds. AF044285 DEFINITION ACCESSION

AF044285.1 GI:2832299 Madagascar periwinkle.

VERSION KEYWORDS SOURCE

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Submitted (22-MG-2010) Salk Institute Genomic Analysis Laboratory
(Signal), Plant Biology Laboratory, The Salk Institute for
Balodgical Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Genomic Sciences Center (GSC) members carried out the contection and clustering of Nat. Consection Nov. Farkon Architopess Pull-Length CDNY.): SekI.M. Membeka.M. ishida.J., SakI.M. Mempeka.M. ishida.J. Hayashizaki.Y. and Shinozaki.K. Carninci.P., Kawai.J.
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Arzi H.E., Gisselment, C., Schilfmenn, S. and Schwenn, J.D.
A cDM, Ecc adentyl, Sulphte (ASS)-kinase from Arabidopsis thallana
Boochm. Biophys. Acta [218 (3), 447-452 (1994)
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/BC_unabe="2'r]-2'r]-2*
//bC_unabe="phosphozylate=3'-0H group of adenyly1sulfate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chodon, sister, 1958 kinase

Product 1958 kinase

Moresel-Carlo 1958 kinase

The Carlo 1959 kinase

The Carlo 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCLAPSK 1185 bp mRNA linear PLN 05-FEB-199
A.thaliana (L.Heynh.) chloroplast mRNA for recombinant APS-Kinase.
X75782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta:
Spermatophyta; Magnollophyta; endicotyledona; orre endicots;
Nosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
320 GluCysProSerProLysAlaMetAlaLysGlnValLeuCysTyrLeuGluGluAsnGly 339
                                                                                   849 GGAGGAACTICICCTATCGAAATGCCGGAAAAGCTGGTCGGATACTTACATAACAAGGGT 908
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Submitted (03-Nov-1953) Schwenn J. D., Ruhr University Bochum,
Biology, Universitaetsstr. 150, 44780 Bochum, Germany
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Arz.H.E. Gisselmann,G., Schiffmann,S. and Schwenn,J.D.
Ar. A. E. Alboroplast APS Kinase CDNA from Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APS-kinase; ATP:adenyly, sulfate-3'-phosphotransferase
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/db_xref="taxon:3702"
/clone="Pk139x14cDNA"
/tissue_rype="leg"
/clone_llb="cDNA in lambda ZapII"
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42. .872
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3 (bases 1 to 1185)
Schwenn, J.D.
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Products—"A: Rag 14750/Prock 2.11"

Crons In City—"A: AMA 1659 C.11"

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200 LeukspülykspaksileukrgHisGlyLeuksnargkspieuSerPheLysklaGluksp 219
409 CTTGATGGTARANTSTRAGGATGGCTARAACGTGGTGTAAACGTGAGAT 554
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Oy 235 Db 16474	Qy 255 Db 16534	Qy 267	Db 16594	Oy 268			0y 296	Db 16774							Oy 319 Db 17013	0y 339	Db 17073	RESULT 10 AB013390 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS	SCURCE		REFERENCE AUTHORS	TITLE	JOURNAL	REFERENCE AUTHORS	TITLE		COMMENT

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Complement(join(2419, .24249,24339, .24923))
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/dd xref="G::9757870"
/translation="MATNNIVRLIAPSRSVSSRPLEPVSRPLSSGTPPPPQAPSPWQD
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ALKRGGVHAADWTQYKYKMLEDVXIDTDSSVLTTVTLTEILDSTKALASFKYDDN
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YAIDHSTAVKAKLNNHGTLGALLOHEVLPRSLVTVSSEIDTKALEHPPFGLSFALRP
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21129 - 121216,11301, 21376, 24772, 21830, 21907, 22163,
22256 - 22544, 24620 - 22730, 22866 - 23044)
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/product-adenylsuliate kinase-like protein"
/protein_id=mbm09460_1"
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strong similarity to unknown protein"
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econ (Amberral)  1177. 13914  (Amberral) 17.00	Alignment Scores: 2.56-19 Longth: 11827 Prod. 50. 1 Control 11827 Score: Smallerty: 0.55 30 Control 1182 Score: 0.55	US-09-70-184.4 (1-343) A MYSSJ7 (1-11826) C (1-12426)	Bb 57846 CTTCANCANANGGOTTGGTCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGTTGGATCGATC	0 20 Clyspotrational (1916) [11] [11] [11] [11] [11] [11] [11] [11	0g         227           12.808         TYACHANTOATAACAATTOTTIAAGGGTTTAAGGTAATAGTTTS 31145           0g         228           128         TATAAGAGAATTOATAATAATAATAATAATAATAATAATAATAATAAT	09 215 Alangha Leipy Hillego Hillehaser Louis Heererory Argapanty app 244 bb 1926 of The Cheffel Hill Hill Hill Hill Hill Hill Hill Hi	09 286  DD 58325 TACTIVATANGAMITHOCITECTHATAAAANAMATATAAACAMATAAAAAAAAAAAAAAAAAAA	Oy 282 Protysolytuserytuseskiakiakighticilytisilatisi Db 58445 Cockhologostytakidhtitiotistockoposiolokakirokakogrintocchakakakan 58504 Oy 285
Agence 12317.20°  exon // Agence 12317.20°  // All 12317.20°  // A	ocon 7822.7.28696  Intron 7822.2.2899  American 7823.2.299  Con 7822.2.29			Inition 7889.7 (1999)  Roon 7889.7 (1999)  Roon 7889.7 (1999)  Roon 7889.7 (1999)  Inition 7098.7 (1997)	econ 30428-2111 //master-1517-10 //master-1517-10 //master-1517-10 //master-1017-10 econ 30466-30623		ALTON (ADDR-13.11)  REON (ADDR-13.13)  REON (ADDR-13.13)  ADDR-13.13(ADDR-13.13)  ADDR-13.13(ADDR-13.13)  ADDR-13.13(ADDR-13.13.13)	econ 3412-13150 1412-13150 1417-0 1518-1317.20 1417-0 1618-1317.20 1618-1317.20*

10	190   1916   1917   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1918   1
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WP059523         MARCH INDEX         PLM 20-ULL-1998         OF 202 GL           Oncernoscribal intentinal 10.7 bp. mark         Linese mRNA, complete         OF 222 GL           AF059523.         T1310470         DD 00 CG         DD 322 GG           Distriction and intentinal	
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Marking associated interactions   Marking associated interactions   Marking associated interactions   Marking associated   Marking as	OHIS-SerAsnPhelleGluVulPhelleAspLeuProLeuLyslleCysGluAlaArgA 281
Black Calculation   Balance   Bala	281 spProtysGlyLeuryrLysLeuAlaArgThrGlyLysIleLysGlyPheThrGlyLleA 301
1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1.107    1	301 spAspPrOTycGubroProlleAmnGlyGlulleValItleIysWetLysAspCu 319
Macron   Macro   Mac	-GluCysproSerProLysAlaMethlalysGluValLeuCysTyrLeuCluGluAsnG 339
RESULT 14 ATACO09540 LOCGS	EUSAGSCUATGSCGAAGCAGATCTTTGACTATCTUGAGGGGGGGGGGGGG
DEFINITION	ATACO09540 101410 bp DNA linear PLM 24-3DM-2001 ATACO09540 brailone chromosope 111 BAC F20823 genomic sequence, complete sequence.
WEST	0009540. G. GI:12408711 G. Cress.
Management Scores: 1-58=20   Length: 1017   Registering Expressed Strategic Strategi	Bharyord, Virtidiplandes Erseptophysis Bharyophysis Teschophysis generophysis almost help and confident and confident and confident in 1. (Season 2.0 2014) or maintained a measurement of the 1. (Season 2.0 2014) or "Town C.D. mellion". The Care of the Bennish C.M. Mook H. "Syllics", Verdebock T.E. Santanedok M.E., Robinskie T.M. Mook H. "Syllics", Verdebock T.E. Santanedok M.E., Robinskie T.M. Son W. "Syllics", Verdebock T.E. Son W. "Syllics", Verdeboc

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	HGHSPAVVTGKPIDLGGSLGRDAATGRGVLFATEALLNEHGKTISGORFAIQGFGNVG
	SWAAKLISDKGGKIVAVSDYTGAIKNNNGIDILSLLEHAEENRGIKGFDGADSIDFDS
	ILVEDCDILVPAALGGVINRENANBIKAKFIIEGANHPTDPEADBILKKKGVMILPDI
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	/note-"exon predicted by xgrail, quality marginal"
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Best Local Similarity: 3
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DB: Alignment Scores: Pred. No.:

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	ACCESSION VERSION KRYWORDS	
_	SOURCE	Clostridium acetobutylicum.

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	LOSETIONN D. 1131) 1 (Dessel Too 1113) NOLLING J. REFORM C. Omelchemko, M. W. Markarova, K. S., Zeng, O., Seng, O.,	Daly W. J. Mementi, G. M. Yocolin, P. V. and Smith, D. R. Genome Sequence and Comparative Analysis of the Solvent-Producing Description Comparative Analysis of the Solvent-Producing Description Comparative Analysis (2001).	21359325 1166286 2 (bases 17 1131)	Childress, D., Zeng, O. and Smith, D.R. Direct Submission Submitted (24-UU_2001) GTC Sequencing Center Production,	Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100 Beaver Street, Maltham, Ma 02453-8443, USA Location/Onalifiers		/STRINE ATC: 824 /db_xref="ATC: 624" /db_xref="taxon: 1488"	2711665 /gene="CAC0101"	2711665 /gene="CAC0101"	/codon_start=1 /transl_table=11		/db_xref="G1:15022926" /translation="MSPDSMCETBMTTPSWLISHTINGUNTEMITED&RYS	KKRGDISALLOIM "RKKOSMATIKNITI TRAALISALLITUVALTITYV VERTETRAKIS KKRGDISVECTRIKVINSLKOLISALTITUVALTISALLISALTITYV VERTETRAKIS ALVANITALITARIA	DRINGLERALDINGER TO THE TRANSPORT TO THE TOTAL THE DESTRUCTION OF THE TOTAL THE THE TOTAL THE THE TOTAL TH	GPETPGEVYRIEDSYKNINTENSKANAGSMKVSKEIKEFSIISDKIRLFTEKSKISV MNIDETINTORFORFRATANENSKYNGSPITTETTEKSKYNSV	DVDY TERROR DO THE TOTAL TO THE		/gene="CACOLOZ" 2025, .3254	/gene="CAC0102" /codon_start=1	/transl_table=11 /product="0-acetylhomoserine sulfhydrylase"	/protein_id="Aak78087.1" /db_xref="G1:15022927"	/translation="MKFSTKLIHGNYNLBNTGATNVPIYKSNAYAHSSPQELBNVFKG KFPGYVYSRFSNPTVLEPERRMASIEGGLTATSAASGMSAIYMAITNIVHFGDELIAS	TGLYGGTYTLISNLONIGVKVIFLEDISKKTLLNNINENTKLYTETIGNPKLDILDI ESVGRYCKEKGIIFMVDSTISTPYLINDSKYGADVIIHSTSKYINGTSNAIGGMIVDC	GSEKYKHRYENFOKYAEKYDKLAFTAKLKSTSGLDIGASMSPNAELSLTGIETLSL RMKKHCKNAKLASYLKKSDKYTNVNYPHIKSSKYVDIGAKYYDGASGLITPRIGTK	ENAYFLAKLKILLDTTNIGDCKTIIIHPASTICINNTEEBREKAAVYDDLLRLSVGI	3264366	/gene choose	/gene=".cool03"	/codou_statt=1 /transl_table.	/protectd=_non_illocationillocation/ /brotectd=_non_illocation/db_xref="cr:15022928"	/tabelation="mankgyfnyworpktrromankgynymertrogssskgy vasalektybrotythodonlrgglssdpyrstriropspyrteragis ittitetispetednimarilgadpovevytocpischegokgyyrrangeinep
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November 2, 2002, 01:54:13 ; Search time 197 Seconds
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Copyright (c) 1993 - 2002 Compugen Ltd
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(without alignments) 2989,348 Million cell updates/sec 1826 1 RPFHFINGTEPLVTHTQQPP......PKAMAKQVLCYLEENGYLQA 343 US-09-720-384A-4 Perfect score: Sequence: Title:

BLOSUM62 Xgapop 10.0 , Xgapext ( Ygapop 10.0 , Ygapext ( Fgapop 6.0 , Fgapext Delop 6.0 , Delext Scoring table:

Total number of hits satisfying chosen parameters: 1736436 segs, 858457221 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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ALIGNMENTS

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E E	Corn Adenylylsulphate kinase-2 cDNA clone.
X X X	Adenylylsulphate kinase; Adenosine-5'phosphosulphate kinase; APS kinase; 3'-Phospho-adenosine-5'phosphosulphate; PAPS; sulphate assimilation;
X.	corn; clone p0016.ctscj40rb; transgenic plant; screen; antibody; ss.
X S X	Zea mays.
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The present sequence is a cook encoding corn adenylylaulphate kinase (MPK kinase) and softonine 27 (Popphosalphate kinase, This is shooted, and a side content of the present in the conversion of a demonstrate of present in the catalyses the conversion of adenosine 25 (Pophosalphate (APS) to 3 (Pophosalphate in Conversion of a signification of the conversion of the conversion of a signification of the conversion o
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13-JUL-1999;
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The present sequence is a cond encoding when demptylicaliphter kinese. (MS Kinese), also known as adenosture's phosphosulphase kinese, this is obtained from a day add light groun when close with politic sed destructions of a sulphase. Such control sendings, wit could library, MS kinese is a sulphase, prosphosulphase (MS) to 'Prompton' destruction' and a sulphase. This sequence is used as a proble and primer too identify, obtain and synthesize sulphase suppless suppless assulption proteins from other plants. It is also used to produce transpentic plants, that we usefull for altering the expension of the country of New nucleic acid molecule and chimeric gene encoding an adenosine-5' phosphosulate kinase, useful for altering expression of sulfate assamilation protein in plants. Claim 3; Page 34-35; 42pp; English. assimilation protein in plants

DUPO ) DU PONT DE NEMOURS & CO E

14-JUL-1998; 13-JUL-1999; 37-JAN-2000

99WO-US15809. 98US-0092833.

US-09-720-384A-4 (1-343) x AAZ50159 (1-890)

Indels: Gaps:

887.00 84.23% 77.03%

Similarity:

Query Match: Best Local

Score: Percent Similarity:

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Falco SC, Allen SM, Anderson

WPI; 2000-182430/16.

P-PSDB; AAY44792.

306 GCCGAGAACATCCGCAGAGTAGGGAAGTAGCGAAGCTGTTCGCCGACGCTGGCCTCGTC

161 ProHisSerAsnPheileGluValPheileAspLeuProLeuLysileCysGluAlaArg

161 LeuLeuGlyGlnLysGlyCysValValTrplleThrGlyLeuSerGlySerGlyLysSer 126 CTGCTGAAGCCAGAAGGGCTGCGTGTGTGGATCACTGGCCTAAGCGGTTCAGGGAAAAGC

/product= "Wheat APS kinase-1" /note= "Derived from clone wrl.pk0101.e2"

/\*tag= a /product= "

WO200004165-A1.

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936
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Best Local Similarity:
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                                                   Glycine
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                                                                                                                                                                                                          131 1LysGluLysProValMetSerAsnIleGlyLysSerThrAsnIleLeuTrpHisAsnCy 151
                                                                                                                                                                                                                                                                                           eThrGlyLeuSerGlySerGlyLysSerThrLeuAlaCysAlaLeuSerArqGlwLeuHi 191
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                                                                                                                                              GGCGGACGCAGGGGAGAGGATGGCGGGGTCAGAAGCCGTGCCGGTGGTGGCTGTGCC--- 64
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Conservative:
Mismatches:
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285 A: 168 C: 250
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                                                              Best Local Similarity:
BP:
                                                 Percent Similarity:
Sequence 928
                  Alignment Scores:
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When present sequence is a comb encoding sequence after these (APS Kinssen), also known as adenostice? Protophonishtek Kinssen, also known as adenostice? Protophonishtek Kinssen entroping podes adopt callow flower as supplies as settle and the protection. The restly year for now restlet of time special by the restly year for now restlet of a supplies as settle and to protect in this restly year for now restlet of adenostice? Protophon adenostice? The special by the restly year for now restlet of adenostice? The protophon adenostice? The settle are useful for producting attituded are useful for producting attituded are useful for producting attituded as the settle age of the clouse.
Adenylyjaulphate kinase; Adenosine-5'phosphosulphate kinase; APS kinase; so Phospho-adenosine-5'phosphosulphate, PARS; sulphate asamiliation; so'ybban; cione dap2c.pkil3.ali; transgenic plant; screen; antibody; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule and chimeric gene encoding an adenosine-5' phosphosulfate kinase, useful for altering expression of sulfate
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                                                                                                                                                                                                                                                                                                                                       /product "Soybean APS kinase"
/notem "Derlved from clone sdp2c.pk013.all"
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0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999 0007-1999	sim Sim	-384A-4 (1- MetSerAsnI        : ATGTCGACAG	Asparggl:::      GAAAGGCA	SerGlyLy              CAGGGAA	ThrTyrval :::   ::: TCATATATT	AlaGluAsp. 	Aladlyval 	ArgalaLe	CysGluAle            TGTGAAGC	PheThrdl 	AspGl
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	물울 남음물	137	157	177	197	217	301	361	277	297	317
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GluksnClyTyrLeuGln 342 ::: Il:::  I : GlokakdsTyrCryCh 618	7 6 AAA35688 standard; DNN; 1175 BP.		17-OCT-2000 (first entry)	Arabidopsis thaliana DNA fragment SEQ ID NO: 14353.	Hybridisation assay; genetic mapping; gene expression control; protein indentification; signal transduction stray; memberal; asthory;	medacare pacina; promocer, cerminarion sequence; ss.	EP1033405-A2.	06-SBP-2000.	25-PEB-2000; 2000EP-0301439.					06-APR-1999; 99US-0128214, 06-APR-1999; 99US-0128714,								14-MAY-1999; 99US-0134221. 14-MAY-1990; 99US-0134270				 				.0-JUN-1999; 99US-0138540.	

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736 AGGGMTCAAAGGTTTTAACAAGGTTGTGTGAAGAAAAACATTTAACGGG 795 300 TleAspAspProTyrGluProProIleAsnGlyGluIleValIleEysMetLysAspGlu 319 796 ATGGATGACCTTACGAGCCACCATTGAACTGCGAG-----ATTTCTCTAGGACGTGAA 849 320 GluCysProSerProLysAlaMetAlaLysGlnValLeuCysTyrLeuGluGluAsnGly 339 850 GGAGGAACTTCTCTATCGAAATGGCGGAAAAGGTCGTCGGATACTTAGATAACAAGGGT 909 AAC45659 standard; DNA; 1183 BP. 340 TyrLeuGlnAla 343 910 TATCTTCAAGCA 921 AAC45659:

Arabidopsis thaliana DNA fragment SEQ ID NO: 47294. 18-OCT-2000 (first entry)

control; Hybridisation assay; genetic mapping; gene expression ( protein identification; signal transduction pthway; mestabolic pathway; promoter; termination sequence; ss.

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control;

US-09-720-384A-4 (1-343) x AAC45659 (1-1183)

100 GlyAlaArgThrHisCysHisArgGlyIleGlyArgTrpValArgArgArgArgAsn 119 221 GGATCTCAAACTCTGAGTCATAACAAAAATGGATCTATTCCTGAGGTTAAATCCATTAAC ò qq à

159 120 GlyAlaAlaProGlyGluAlaProHisSerProValLysGluLysProValMetSerAsn 139 281 GGT----TIGICIACG 316 q ò

140 IleGlyLysSerThrAsnIleLeuTrpHisAsnCysLeuIleGlyGlnSerAspArgGln

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300 IleAspAspProTyrGluProProIleAsnGlyGluIleValIleLysAspGlu 319 셤 g ò ò

320 GluCysProSerProLysAlaMetAlaLysGlnValLeuCysTyrLeuGluGluAsnGly 339 851 GGAGGAACTTCTCCTATCGAAATGCCGGAAAAGGTCGTCGGATACTTAGATAACAAGGGT 910 TyrLeuGlnAla 343 g ò

990S-0139454. 990S-0139455. 990S-0139456.

Hybridisation assay; genetic mapping; gene expression oprotein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 67599 99US-0135124. 99US-0135353. 99US-0135629. AAC51190 standard: DNA: 714 25-PEB-2000; 2000EP-0301439 99US-0121825 34768 99US-0134941 99US-0137528 99US-0137502 18-OCT-2000 (first entry) 990S-013 99us-01 Arabidopsis thaliana 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 1990 - 19 EP1033405-A2 06-SEP-2000 AAC51190; 

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US-09-720-384A-4 (1-343) x AAC51190 (1-714)

US-09-720-384A-4 (1-343) x AAZ98337 (1-917) ò g ò g ô 90 ò a ò 8 ð Q ð 8 ò 8 ò ó Environmental stress; plant; transgenic plant; anaerobic; flooding; cold; dehydration; drought; heat stress; salinity; osmotolerance; ds. 197 ThrTyrValLeuAspGlyAspasnLeuArgHisGlyLeuAssArgAspLeuSerPheLys 216 360 421 CCGTATAGAAAAGACCGTGACGCCTGCAGGGAAATGATACAGAATTCATCTTTTATTGAG 480 481 GITITCATGAACATGICTCTGCCAATTGTGTGAAGGAAGGAAGGCCCTAAAGGCCTATACAAG 540 541 CTISCACGISCAGGAAGAICAAAGGITTCACAGAATAGAIGAICAGGAAGAGTICACC 600 SerGlyLysSerThrLeuAlaCysAlaLeuSerArgGluLeuHisCysArgGlyHisLeu 196 248 ProTyrArgArgAspArgAspAlaCysArgAlaLeuLeuProHisSerAsnPheIleGlu 267 268 ValPheIleAspLeuProLeuLysIleCysGluAlaArgAspProLysGlyLeuTyrLys 287 288 LeualaargThrGlyLysIleLysGlyPheThrGlyIleAspAspProTyrGluProPro 307 308 IleAsnGlyGluIleValIleLysMetLysAspGluGluCysProSerProLysAlaMet 327 181 TCATATATTCTTGATGGTGACAATCTTCGTCATGGTTTGAACAAGATCTTGGTTTCAAC 241 GCAGAGGATAGAGTGGAAAATATACGCAGGGTCGTTGATGAAAGTCTGATTCCGAAGAAA AlaGluAspArgAlaGluAsnIleArgArgVal-----227 301 CTCACTAATACAAATGCAAATCCTTTAAAAAGGTGTCTCATATGTAGTGATAGTTTACAT 228 GlyGluValAlaIysLeuPheAlaAspAlaGlyValIleCysIleAlaSerLeuIleSer A. thaliana gene involved in environmental stress tolerance. 328 AlalysGlnValLeuCysTyrLeuGluGluAsnGlyTyrLeuGln 342 661 GCTGAGGAAGTGATCTTATCTAGAAGACAAAGGTTTCCTTCAA 705 (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG AAZ98337 standard; DNA; 917 BP 99WO-EP05652 98EP-0202634 (first entry) Lee JH, Verbruggen N; Arabidopsis thallans. WO200008187-A2. 04-AUG-1999; 34-AUG-1998; 14-JUN-2000 17-FEB-2000. AAZ98337; 22 217 qu g g a ò ò ò à 8 à a à 8 à g ô 8 ò

The invention calcate of calculation of could sequence analysis enter involved in Defence to environmental stress in plants. This sequence (AAMS900-2685) are useful for producing a transparint plant having enhanced tolerance or resistance to environmental stress conditions such as nanecologic (Todonia -O.), delydeful tomor drought, leaf attess or salinity. This is useful for producing improved years of great in the salinity of the producing improved years of great in the hard and a such producing improved years of the salinity of the producing improved years of the hard and produced in the induced operators. Sequence SANASSOS 515 seprement producing environmental stress Loterance. isolation of polynucleic acids useful for producing transgenic plant by isolating genes involved in tolerance to environmental stress Claim 4; Page 218-220; 312pp; English.

Sequence 917 BP; 244 A; 220 C; 229 G; 224 T; 0 other;

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ALLQUINGIL SCOLES:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	

40 ProThrProThrLeuAlaValIleLeuValAsnProGlnArgAlaProProVal-----

20 14 CCGTCGGATTCAATGGAAGGATTAGCTATCAGAGCATCTCGA----CCGTCGGTTTTCTGT 58 ---LeuproGlyLeu------Pro

290 ------AAAGAG------AAAGAG

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                                                                              US-09-720-384A-4 (1-343) x AAC51315 (1-483)
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85.09%
72.67%
33.82%
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                           Percent Similarity:
Best Local Similarity;
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158 301 194 421 23 AlaAspAlaGlyValIleCysIleAlaSerLeuIleSerProTyrArgAspArgAsp 254

Mikita T:

Porter GJ,

Seilhamer JJ,

Somoqyi R, Lawn R,

Shiffman D,

Mon Nov 4 12:27:00 2002

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542 GCAGATGCTTAGTGTGCATCACAAGTTCATATCACTTACACTTACAGTGAGGATCGCAAC 601	255 AlaCysArgAlaLeuLeuProHisSerAsnPhelleGluyalPhe	289 Ileaspieuproleuiysilacyscilualaargakspirolysciyleuryriysieuula 289 IIII	309 AgrhicitylsileiysölyPherhicityileAspAspProfytGiuProProlleAsn 309 Agrhicityliliiliiliiliiliiliiliiliiliiliiliiliil	310 GlyglutleValileLysMetLysAspGluGluCysProSerProLysAla 326	327 MethlalygGinValleuCysTyrLeuGluGlu 337 	Search completed: November 2, 2002, 03:08:48
542	255	270	290	310	327	ch co time
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119 6.5 2499 3 16-01-602-6488-1   Sequence   117 6.4 1647 1 10-01-07-3184-9   Sequence   117 6.4 1647 2 10-0	117 6.4 1647 3 105-0628-0534-9 Sequence 9 A R 1 1	6.4 2088 2 18:08-648-69-66-10 Sequence 6.4 2088 2 18:08-777-653-10 Sequence 6.4 2088 2 18:08-579-69-10 Sequence 6.4 2088 2 18:08-576-38-10 Sequence 6.4 2088 2 18:08-576-38-10 Sequence 6.4 2088 2 18:08-26-28-10 Sequence	117 6.4 2008 1 00.5 10.5 40.5 20.4 1.0 Sequence 10. 117 6.4 2008 1 00.5 10.5 20.5 20.4 1.0 Sequence 10. 117 6.4 2008 1 00.5 10.5 20.5 20.5 1.1 Sequence 10. 117 6.4 2008 4 10.5 10.5 20.5 20.5 20.5 1.0 Sequence 10. 117 6.4 2499 1 00.5 10.5 20.5 20.5 20.5 1.0 Sequence 1.0. 117 6.4 2499 1 00.5 10.5 20.5 20.5 20.5 20.5 20.5 20.5 20.5 2	C 43 117 6.4 2494 4 18-00-777-379-3 - Sequence 1, Appl. M.1.00MBPTS 1 Sequence 1, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 3, Ap	APPLOANT: Inlinan, while t. APPLOANT: INLINAN, while philip R. I APPLOANT: Gooder, Ann J. J. APPLOANT: Cooley, Mail C. I APPLOANT: Cooley, Mail C. CORRESCOME COOLEY, MAIL C. CORRESCOME COOLEY, MAIL C. APPLOANT: COOLEY CO	CITY: Palo Alto STAFF: CA COMPATE: CA COMPATE: REALORED FOR CA COMPATE: REALORED FOR CA COMPATE: LINK COMPATE: LINK CAPE COMPAT	SOFTWARE TRANSPACE OF MAINTENANCE VERTION 2.0 CURRENT APPLICATION FOR MAINTENANCE OF THE CALCULATION FOR ADMINISTRATION FOR THE CALCULATION FOR TH
Copyright (c) 1935 - 2002 Compagen Ltd.  OM protein - nucleic search, using frame_plus_pA model  Nun on: Movember 2, 2002, 01:571.19   Swarth mile figeconds  1891.572 William cell updates/sec	PATACE: US/05/27/3844-4 PATACE: US/05/27/3844-4 Sequence: 18/05/27/3844-4 Secring table: BLOSTEN/07/27/27/27/27/27/27/27/27/27/27/27/27/27	Searched: 33333 seqs. 122816752 residues Total mumber of hits stiefying choken parameters: 767066	Maximum DB seq length; 2000000000 Post-processing: Militam Watch Op. Listing first 15 summartes	Comment Line parameters in parameters and parameter	Database : Issued_Patents_BA.*  1. (Agric_Patents_BA.*  1. (Agric_Patents_AA.*  1. (Agric_Patents_AA/Inst@LONE.seq;  1. (Agric_Patents_AA/Inst@LONE.seq;  5. (Agric_Patents_AA/Inst@LONE.seq;  5. (Agric_Patents_AA/Inst@LONE.seq;  6. (Agric_Patents_AA/Inst@LONE.seq;  6. (Agric_Patents_AA/Inst@LONE.seq;  6. (Agric_Patents_AA/Inst@LONE.seq;  6. (Agric_Patents_AA/Inst@LONE.seq;  7. (Agric_Patents_AA/Inst@LONE.seq;  7. (Agric_Patents_AA/Inst@LONE.seq;  8. (A	Free; No. 15 the Instance of results predicted by Chance to have a serve apparer than or equal to the score of the result beauties, and individual or the score of the result beauties.  Result Score March teacher in in the score of the result beauties.	20.7 1366 1 100 00 00 00 00 00 00 00 00 00 00 00

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496.00
60.83%
45.42%
27.16%
                                                   INFORMATION FOR SEQ ID NO: 4:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2506 base pairs
TYPE: nucleic acid
                                                                                                                    single
                                                                                                                                                                   LIBRARY: LUNGNOTO2
CLONE: 373887
                                                                                                                                     linear
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Best Local Similarity:
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Podersen. Nogens Bohl
Sorensen. Steen Beth Goodling a composite
INVERTION: Extracted beverage vising genetically modified yeast
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SOFTAMBE: FBSLESSO, FOR Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <Unknown>
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/153,310
FILING DATE: 15-Sep-1998
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: <Ur
                                                                                                                                                                                                          CORRESPONDENCE 42
CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington
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Sequence 41, Application US/09153310
patent No. 6326184
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-672-5300
TELEFAX: 202-672-5399
                                                         APPLICANT: Glermansen, Claes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1160 base pairs
                                                                                                                                                                                               atrains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                Hansen, Jorgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.47e-32
475.00
66.85%
53.80%
26.01%
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                                                                                                                                                                                                                                                                                                                                 USA
                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          STATE: DC
                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                        TITLE OF
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Alic	Alignment Pred, No.:	Scores:	00236	Length:	6803	
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Best Ouery DB:		Local Similarity: Match:	26.79* 8.49* 3.49*	Conservative: Mismatches: Indels: Gaps:	886 13	
ns-(	09-720	-384A-4 (1-34	3) x US-08-665-25	59-19 (1-6803)		
ολ	14	ThrHisThrGlnG	InProProSerProAl	LaProGlyProAlaSe	ThrHisThrGinGlnBroProSerProAlaProGlyProAlaSerGlnGlyGlnArgGln	33
a	2555		AGCCCCTTCCCCGCT	rescccasccccccr	TGAATCTGCTTCTGAT	2614
6	34		euSerProThrProTh	or Leu Ala Vali le Le	GlyAsnThrLeuLeuSerProThrProThrLeuAlaVallleLeuValAsnProGln-Ar	53
g	2615		ATGAGGCCCCCTCC	recreecended and	TCCCGACCCGAGCAGC	267
67	53		9AlaProProValLeuProGlyLeuThrProSerAspAlaProLeuProAl	ProSerAspAlaProI	.euProAlaLeuValIl	7.3
g	2672		GGGCCGGGCTTGCGC	CTGCTGCGCCCCCC		272(
ò	73		ProArgSerSerHiss	SerSerAlaGlyLeuA	eHisGlyLeuThrProArgSerSerHisSerSerAlaGlyLeuAlaSerAspSerGlyAr	63
q	2721		TCCTGGCACA	AGCTCGTCCGCCCTCG	TCCTGGCACAGCTCGTCCGCTCGCTGCAGCCGGGAGGAG	276
ò	93	gArgGlu				95
Q	2762		CACCGCAGGCCCGGC	CCCCACGCCCTTC	GGGCGGCCCGTGCACCGCAGGCCCGGCCGCCACGGCCCTTCCCGGGAGGCCGGGAGA	282]
οy	95					95
q	2822	8	ACCCTCGGTGGGTGAG	STGCGAGCGGCGGGTG	#GCTCCGCCCCGGCCCTCGGTGGGGTGAGCGGCGGGTGGGGGCCTCCGCGGGCGG	288]
ò	96			scysHisArgGlyIleGlyArg	IleGlyArgTrpVa	113
QQ	2882		GACGCC	NGTCATCGCTCTAGGC	CCAGCGGGAGGAC	293
0y	113		largargargargasnGlyalaalaaroGlyGlualaProH	ProGlyGluAlaProH	isserProvalLysGl	133
QQ	2936		CGCTGCTGTGCTGGGC	-SCCGGGGGGGGGGG-		2978
οy	133		SerAsnileGlyLys-		uLysProValMetSerAsnIleGlyLysSe	143
g	2979		CCACCTCTGGGCCGGG	3CTGGGGCCGCCCGGG	SGCCCTGTTCCTCGGC	3034
6ò	143	rThrAsnileLeuTrpHi	TrpHisAsnCysLeuI	TleGlyGlnSerAspA	sAsnCysLeuIleGlyGlnSerAspArgGlnLysLeuLeuGl	163
g	3035	ATTGCGGGCCTGGTGG	1	GCAGAGCCGC	GCAGAGCCGCGGAGAGGCCTTCTTT	3076
οy	163		valval	TrpileThrGl	yleuSerGlySerGlyLy	179
q	3077	CCCCAAGGGCAGC	CCCCAAGGGCAGGTCTTGGGGCCCGGCC	ACTGGCTGACC	GCAGCGGCTCCGGCCA	313
ò	179	SSerThrLeuAlaCy	sAlaLeuSerAr	gGlubeuHisCysArgG	GlyHisLeuThrTyrVa	199
g	3134	CTGGCTGGC			CTGGGGGCTGC	312
٥y	199		AsnLeuArgHisGlyL	-euAsnArgAspLeuS	lLeuAspGlyAspAsnLeuArgHisGlyLeuAsnArgAspLeuSerPbeLysAlaGluAs	219
g	3158		AGGCACGCTC	TTCGCCGCCCTGAGT	сстевессосовесе	3208
οy	219		pArgAlaGluAsnIleArgArgValGlyGluValAlaLysLeuPheAlaAspAlaGly	SluValAlaLysLeuF	24	38
g	3209		CCGCCGACCCCTGCCACGATGAGGGGGTGCGCCCCCGCGGCTGCGTGCCAGGACTGGT	recoccececerac	m	992
RESULT US-08- : Segu ; Pate ; GEN	JLT 4 18-762 squence ttent t SENERAL APPL APPL APPL	ESULT 4 S.08-762-500-19 Sequence 19, Application Patent No. 6030806 GENERAL INFORMATION: APPLICANT: Landes, APPLICANT: Burn, Tif	ton US/08762500 Gregory M.			

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2762 GCGGCGGCCCGTGCACCGCAGGCCCCGCCCGCCCACGGCCCTTCCCGGGAGGCCGGGAGA 2821
                                                                                                                                      035 ATTGCGGGCCTGGTGG------GCAGAGCCGGGGGGGGGCTTCTTTT 3076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3077 CCCCAAGGGCAGCGTTTGGGGCCCGGCCACTGGCTCACC---CGCAGCGCTCCGGCCA 3133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 largargargargasnGlyalaalaProGlyGlualaProHisSerProValLysGl 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 -GlyGluGlyArgGlyAlaArgThrHisCysHisArgGly-----IleGlyArgTrpVa 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 uLysProValMetSerAsnIleGlyLys------Se 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 yGlnLysGlyCysValVal-----TrpIleThrGlyLeuSerGlySerGlyLy 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 lLeuaspGlyaspasnLeuargHisGlyLeuasnArgAspLeuSerPheLysAlaGluas 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 rThrAsnIleLeuTrpHisAsnCysLeuIleGlyGlnSerAspArgGlnLysLeuLeuGl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 SSerThrLeuAlaCysAlaLeuSerArgGluLeuHisCysArgGlyHisLeuThrTyrVa 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 pargalaGluAsnIleArgArgValGlyGluValAlaLysLeuPheAlaAspAlaGly 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GARETÉGOS C. CLASS
PERCICANT: GALETÉGOS C. CLASS
APPLICANT: RELIGIO, MAY
APPLICANT: ANILHAY GART
APPLICANT: ANILHAY GART
TITLE OF INVESTICAL GARGETH POLYKETIDE SYNTHASES AND BACOING DNA
TITLE OF INVESTICAL STREEPON.
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Matches:
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CURRENT PAPLICATION NUMBER: 195/104,085
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: 109/010.809
BARLIER FILING DATE: 1998-01-22
NUMBER OF SED ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/09144085; Patent No. 6280999; GENERAL INFORMATION:
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US-09-144-085-3
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SEQ ID NO 3
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27.04%
6.76%
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Best Local Similarity:
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US-09-144-085-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 eHisGlyLeuThrProArgSerSerHisSerSerAlaGlyLeuAlaSerAspSerGlyAr 93
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MARICANT. CORRORS LIGHTLY D.
APPLICANT. CORRORS LIGHTLY D.
APPLICANT: VAN BARY, Treaters J.
TITLE OF TRYBITCH. TO PROPER HIGHAR TREADER OF MAKING AND USING SAME
NUMBER OF SEQUENCES.
OF SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRPLICATION WINBER: US,08/762,500
PILING DATE: 09-00C-1996
CLASSFEIGHTON: 435
PRIOR APPLICATION DATE:
APPLICATION WINBER: US,08/665,259
PELING DATE: IT-70W-1996
PRIOR APPLICATION NUMBER: US,00W-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                 ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: ELOPPY GISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-NOS/Ms-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREEPHONE: (509) 872-8400
INPORTENT (509) 872-8400
INPORTENT (509) 872-8415
SEQUENTION FOR SEQ ID NO: 15
SEQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: IG
TELECOMMUNICATION INFORMATION:
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Framingham
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Best Local Similarity:
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Oy 187 rArgGluLeu 190		g	628 CAGCCCC	628 CAGCCCCGACAGGCC
DD Z6465 GCGTGAGTTG 26474		ζÓ	148 pHis/	148 pHisAsnCysLeuIl
US-09-461-474-5	707 (3700)	q	111 668 -CACC	111 668 -CACCGTTCTTGAGA
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APPLICANT: Allen, Steve	iuc	qq	727 TC	727 TCCTCAACG
APPLICANT: Sakai, Heise ; TITLE OF INVENTION: Plant Metal Transporters	t Metal Transporters	õ	188 rgGlu	188 rgGluLeuHisCysA
; FILE REFERENCE: BB1303 U ; CURRENT APPLICATION NUMB	IS NA SER: US/09/461,474	a	753	
; CURRENT FILING DATE: 1999-12-14 ; EARLIER APPLICATION NUMBER: 60/112,562	99-12-14 50/112,562	0y	208 lyLeu	208 lyLeuAsnArgAspi
; EARLIER FILING DATE: 1998-12- ; NUMBER OF SEQ ID NOS: 17	18-12-16	qq	780	AATGATA
; SOFTWARE: Microsoft Offi ; SEQ ID NO 5	.ce 97	ó	228 1yGlu	228 lyGluValAlaLysL
; LENGTH: 1377 ; TYPE: DNA		qq	823 GCGAG	823 GCGAGGTCAATACTC
; ORGANISM: Triticum mestivum US-09-461-474-5	ivum	0y	243 laSer	243 laSerLeulleSerP
Alignment Scores:		qq	883 CAGAG	CAGAGTTTCTGAGTC
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larity:	tive:	g G	943 TCGAT	943 TCGATACCCACTCCA
		Qy	254 spAla	spalaCysArgalaI
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۵	Db 823	GCGAGGTCAATACTCAGTTCCAGGACGCTGAACTCACCACCTTTGTCTGTGTGTG
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۵	Db 943	TCGATACCCACTCCATCGTTGTCAACCAGCTGCTCTTCCCCAAGAAGGCTAGCGATTGCC 1002
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۵	pb 1123	AGAAGCTTGAGAAGTTTAGTGAAATGCTTGTTACAC 1158
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CURRENT APPLICATION DUTA; APPLICATION DUTA; APPLICATION WINNER: US,006/156,020 ATTING DARFIE: 13 ATTING APPLIES: 13 ATTING APPLIES: 13 ATTING APPLIES: 13 ATTING APPLIES: 13,142 RESTRUCTION WINNER: 13,142 TRADRACT CREATE 400 MBH: 3,413 TRADRACT CREATE 400 MBH: 3,413 TRADRACT (13) 115;112;1100 TRADRACT (13) 115;112;1100 TRADRACT (13) 115;112;1100 TRADRACT (13) 115;112;1100 TRADRACT (13) 1100	TITE:metate candours  TITE:metate candours  MATINESTICAT:   Jan.    ANTISERICAT:   Jan.    ANTISERICAT:	DOTRE   FEBRUARY TON:   CASE   CASE	NAME/CRIS materiors, we have a construction consists in a nucleotide of CHERA TORONAME AND ASS. White materior consists in a nucleotide of CHERA TORONAME ASS. White materior is a freeting 253 of the native raq pack of CHERA IMPOSATION collections and Feeting 253 of the native raq pack properties on conservative.    NAME/CRIS   N	dis-0g-156-020-18   months   moure   moure   mouths   m

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at position 504 of the native Tag DNA polymerase from G to A. which is conservative in nature."
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US-08-156-020-5
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LOCATION: More replace(952, "...")
LOCATION: REPORT MORE Alteration at positions 952 of the native Tag DNA
OTHER PRODUCTION alteration at controlled the sequence of T to C. This results in in
OTHER PRODUCTION: mainto each diamage of Leat to Proc."
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WhatTON: /noche "This mutation regults in a nucleotide
WHATTON: alteration at position 2555 of the native Tag DNA
SMATTON: polymerase uncleotide sequence of G to A. This mutation
SMATTON: conservative.
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Teplace(193, "t")

Teplace(193, "t")

This mutation changes the nucleotide

THANTION: at position 193 of the native fag DNA polymerase from

THANTION: C to T. resulting in an amino acid change of Arg to Cy
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                                     NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff
STREET: 10 South Wacker Drive
HITLE OF INVENTION: Polymerases
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NOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ORIGINAL SOURCE:
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COTREN INTERCRATION. TO INCLE" THIS matation results in a nucleotide

OTHEN INTERCRATION. TO INCLE" THIS matation as positions 95.0 of the mative Twa GNA

OTHEN INTERCRATION: alteration at positions 95.0 of the mative Twa GNA

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APPLICART: Moses N.D., Robb E.
TITER OF TWENTION: Modelited Thermo-Resistant DNA
TITER OF TWENTION: Polymerases
WHORER OF SEGURENCE:
CORRESPONDENT ADDRESS: SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: ATYOMEN/GREY TRESPORT OR ATYOMEN'S CREEKING BY ANNE; CETEBILE OF PLD. MICHORAL S. PERSISTENCY OR HUMBER: 73,142 FLEEFERS, CALLEY STREEKING STREEKI APPLICATION NUMBER: US/08/156,020 E: Allegretti & Witcoff 10 South Wacker Drive Sequence 7, Application US/08156020 Patent No. 5474920 COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh ORGANISM: Thermus aquaticus MOLECULE TYPE: DNA (genomic) CLASSIFICATION: 435 719 CCGATGCCTTG 708 271 Aspleuproleu 274 linear Chicago N.S. õ ORIGINAL SOURCE: FILING DATE: 90909 RESULT 10 US-08-156-020-7/c ADDRESSEE: ropology: COUNTRY: ANTI-SENSE: STREET: STATE: FEATURE 9 qq ò ò g ó à

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1090 GGGCCAGAAGATCGGCCCACATGGGCTCCTTGCGGGAAAGCCAAAGCCCACGAAGGCCC 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 LeuLeuGlyGlnLysGlyCysValValTrplleThrGlyLeuSerGlySerGlyLysSer 180
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----ArgAsnGlvAlaAlaProGlvGluAla 126
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Sequence 9. Application Us/NB136020
Repear No. 547450.
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Reprode 1. NBCPMATON 1. DRAW 1. NBCPMATON 1. NBCP
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OPERATING SYSTEM: Macintosh
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
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10 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 93.413
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TELEPHONE: (312)715-1000
TELEPAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 9:
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MEDIUM TYPE: Floppy disk
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DOWATON: replace(75%, "a").

OTHER INFORMATION: //OCCe=""this mutation results in a nucleotide
OTHER INFORMATION: alteration at position 2535 of the native Tmq DNA
OTHER INFORMATION: alteration at position 2535 of the native Tmq DNA
OTHER INFORMATION: a conservative."
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OTHER NEWBORNION: Once="White materion results in a nucleotide
OTHER NEWBORNION: Attention at position 66 of the matine Twe DNA
OTHER NEWBORNION: attentions.
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OTHER NEWBORNION: anion and change of law to Pro."
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ON: replace(34, "a")

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TREDACHION: Alteration at position 34 of the mative Twa DNA
TREDACHION: Alteration at position 34 of the mative Twa DNA
TREDACHION: Alteration at position by the CP to A. This results
TREDACHION: mainto acid change of PNe to Ile."
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OTHER NHORMATION: A hote-"This mutation results in a nucleotide
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                                                                                                                                                                                                                  LOCATION: resplace(ps. fg*).
OPTRINGNATION: Anote-"This metation results in a nucleotide OPTRE INFORMATION: Anote-"This metation fg by 6 the native fg DNA OPTRE INFORMATION: polymerase nucleotide sequence of C to G."
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Matches:
Conservative:
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E: DNA (genomic)
              : 2626 base pairs
nucleic acid
EDNESS: single
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SEQUENCE CHARACTERISTICS
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OTHER INFORMATION: PERTURE:
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Best Local Similarity:
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MOLECULE TYPE:
HYPOTHETICAL: N
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Mon Nov 4 12:27:00 2002

; COUNTRY: United States of America	COMPUTER REMANSIE FORM: MENDING TYPE: FEOPPY disk	OPERATIVA SYSTEM, PC-TO-SAFE-DS SOFTWARE: PRICENT, PC-TO-SAFE-DS CURRENT APPLICATION DATA: APPLICATION NOMER: US/A04/923,137	FILMS DAYS: FRING PAPE 435 FRING PAPELLARION 435 RECONSTRUCTION NUMBER: US 60/024,700	FILMS DATE: 0.68E-1996 FATORBEY/AGRAT INFORMATION: NAME: BEA, MANE: BEA, BEA, BEA, BEA, BEA, BEA, BEA, BEA,	REPERMINAL/DOCKER THUBBER: GNPN.021CIPJUSA TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 18F008A4710N: TELECOMMUNICATION 225-540-5900	I NOVANICO NO SOLO I DOCI CO SOLO SOLO SOLO SOLO SOLO SOLO SOLO S	1 STANDENBES OUDLE TOPOLOGY: UNIXABAN US-06-202-127-2 FPS: GDNA US-06-202-127-2 FPS: GDNA	32.9 Length: 119.50 Matches:	Percent Similarity: 34.964 Conservative: 23 Beet Local Similarity: 26.324 Missacches: 90 Onery Match: 6.544 Similarity: 3.54 DB: 12	US-09-720-384A-4 (1-343) x US-08-923-137-2 (1-36519)	Qy 19 ProProSerProAlaProGlyProAlaSerGlnGlyGlnGlyAsmThrLeuLeu 38	Db 19881 CCTGOGTGCGCTGGCCCTGGCCCTGCGCTGCTGCGCGCGC	156	S9 ProGlyLeuthrProSerAspAlaProLeuProAlaLeuValllefisGlyLeuthrPro 78	79	Db 15764 GGGGTCCGCCACCACGCTGTCGATGACGGCGTCCACGGGGAGACGGG 15717	GGGGGTGTA	dy 114 ArghrakrakrakrakrakrakrakrakiyalaklaprodlydluklaprovilsGerProvallysciu 133 15672 GARFALCHORGORGORGORGORGORGORACORACORGORGORGORGORGORGORGORGORGORGORGORGORGO	Oy 134 LystrovalbecSerAsniloGiylysSerThrAsnilaLeuTpHisAsnCysLeuile 153  Db 15612 GCCGGAAGTGCCCGGCGAAGGGGGTVTTGCGVAAGC		Db 15567 GGGGGGCCTCCGTACATCTTGCTGGGCGCGCGCAACCGGTGTTATTACTGG 15508
Db 1510 CCACCTCCAGGGACAAGGCCCTGAGATAGGCCACGTCCAGGCGCACCCCCGTGGCCTCCA 1451	Qy         72           12         1450           TOTGGGCCNGGACAGGGGCCTCTCCCCCCCCGGTAAAGCCAAAAGGGCCTTTTTTTT	Oy 78 ProArg8erSerHisSerSerAlaGlyLeualaSerAsp8erGlyArg 93 1390 CTPCCCCTAAGCTTCCCCCAAAGTTGGCSAAAGAGTTCGSAAAGGGGGCCCCT 1331	99 94	Qy 106 HIAN-9G1Y11eCIYAN9TFDVALAC9NF9AR97117 Bb 1270 TGSARAGGTCCAGAAGGTAGGCGAAGGCTAGGGTAGGCGGAAGGC 1211	Qy 118	dy 127 Pro	Oy 141 GlytysSerhkrasileteurpHisAsncysteulleGlyGlnSerkspArgGlnLys 160 Glocomonactosococococococococococococococococococ	09 161 LeuLeuGlyGlntysGlyCysValValTrplleThrGlyLeuSerGlyGerGlyLySSer 180	Oy 181 Thriewilacys/laicuseracgoluicusiscysacgolystscenthrypval 199 1004 TCCACGCCTTCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Gy 200 LeuaspGlyAspAsnLeuArgHisGlyLeuAsnArgAspLeu 213	Db 959 CIGCGAAACICGAGGCICICCGAAAIGGCCCIAAAGCTICICGGGCICGCGCTT 900	dy 214 SerbhelyaklaGlukapārgalaGlukanīlakrgaksyaīGlyGluValālalygieu 233  bb 899 TIGGGGAĀRSCACETCACAGGGGAGGSTGGGTGGTGGTGCTGTGCCTAGGAAAGC 840	Oy 234 PheAlaAspAlaGlyValIleCysIleAlaSerLeulleSerProTyrArgArgAspArg 253	Db 839 TICAGATGGTCCATGTGGGCCAGGATCTTCTCCGGGATGGCGGGCCTTCAGCCGGTCCAGG 780  0v 254 Asnal acvsArchla LanisalProHIRSer Asnaple: Leginval Phatle 270			LD 719 CCGATGCCCTTS / UB	68-923-137-XC Sequence - Application US/08923137 GENERAL No. 603174 GENERAL WO. 603174	APLICANT: Willon, James M. APLICANT: Willon, James M. APLICANT: Erias, Steven F. TYLL OR TWURTION: Chimphrace Adenovirus Vectors TYLL OR TWURTION: Chimphrace Adenovirus	NUMBER OF ERQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSSE ADDRESSSE ADDRESSSE ADDRESSSE ADDRESSSE ADDRESSSE ADDRESSE ADDR	STREET: Spring House Corporate Cntr., P.O. Box 457

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IDENTIFICATION METHOD: comparison to IDENTIFICATION METHOD: sequence in GenBank, Accession number J04639.
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    JeuleuSerProThrProThrLeuAlaVall1eLeuValAsnProGlnArqAlaProPro 56

                                                                                                                                                               AIRTHOSES LANGER F.C., SECHELS, S., MITTHOSES SEALS, R.Y., MARTHOSES GELEGAR D. H. WARRDA, K., Drummond, R., TITLE: ISOSIALION, CHRISTOCHIZATION and THE SECURITY. SECURITY SEASON TO SERVE SECURITY SEASON TO SERVE SEALS SEA
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Best Local Similarity:
COCATION:
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15327 TTTCACT-----GACGGTGGTAATGGTGGGCGCGGG---CGGCCGGACGAGGATCT 15280
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                                                                                                                                     167 ------CysValValTrpIleThrGlyLeuSerGlySer 177
                                                                                                                                                                                                                                                                                                             178 GlyLysSerThrLeuAlaCysAlaLeu-----SerArgGluLeu-HisCysArgGlyHi 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 sLeuThrTyrValLeuAspGlyAspAsnLeuArgHisGlyLeuAsnArgAspLeuSerPh 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 eLysAlaGluAspArgAlaGluAsnIleArgArgValGlyGluValAlaLysLeuPheAl 235
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INDIVIDUAL ISOLATE: YT1, ATCC 25104
IMMEDIATE SOURCE: amplified from genomic DNA
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MEDIAN TYPE: Disected .3.5 inch.
MEDIAN TYPE: Little Back as Ecode (IBM)
OFFERTING STETEM: MR DOS VEREIGN .3.5
CURRENT APPLICATION WAT.

CURRENT APPLICATION WAT.

FILING WATE: 1390;026
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PRIOR APPLICATION DATA: No. 6083686e
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: Bastman Kodak Company,
ADDRESSE: Patent Department
STREET: 343 State Street
CITY: Rochester
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Patent No. 6083686
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REGISTRATION NUMBER: 27,678
REFERENCE/DOCKET NUMBER: 58374
TELECOMMUNICATION INFORMATION:
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TELEFAX: (716) 477-4646
INFORMATION FOR SEQ ID NO: 1:
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COUNTRY: U.S.A.
ZIP: 14650-2201
COMPUTER READABLE FORM:
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US-07-602-848E-1/c
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2499 83 20 124 105

Length: Matches: Conservative: Mismatches: Indels:

Mon Nov 4 12:27:00 2002 us-09-7	us-09-720-384a-4.xni
Db 884 TCCAGGGCCTTGGCAGAAGG	Best Local Similarity: 26.01% Mismatches: 130 Query Match: 6.41% Indels: 89
	Oy 17 GinGinproproserProAlaProGlyProAlaSerGlinGlyGlnArgGlinGlyAssmin 1
Db 800 TCCCGGTCGGGCTCCCCCTTTGGCGAAGTCCACCTCCAGGGGCAGTCGGTGCCCC 741  Ov 227 V31GLVGLUVBLAJALVSLEUPPAAJAASDAJAGLVVATTPCVSTTAJAGATAGCATC  Ov 227 V31GLVGLUVBLAJALVSLEUPPAAJAASDAJAGLVVATTPCVSTTAJAGSTAGLVAT	37
740 TIGGCCAGGTCCCAGGAGCTTCAGATCGTCCAGGATCTTCTCCCGGATG	1432
Oy 247 SerProTyrkrqArgAsphrqAsphlaCysArgAlaLeuLeuProHisSer 263   11	0y 57 Valleuprofijteuffrfrostaphalkorderrahalaeu
Gy 264 AsmpheileGluvalPheileAspleubroLeu 274  Dh 620 AsmpheileGluvalPheileAspleubroLeu 274  Dh 620 AsmpheileGluvalPheileAspleubroLeu 274	Qy 72
SULT 14 -08-073	0y 78 ProArgSerSerHisSerFarAlaGlyLeuAlaSerAspSerGlyArg Db 1273 CCTCCCCCTCAAGCCTCCCCCAAAGGGTGGCGCCGCT
Sequence 7. Application US/USU/3384C. Partent No. 554311 SERRAL INCOMPANION:	Oy 94
APPLICANT: LYMICATION VALOOT.  APPLICANT: BOWN MARY AND STATE OF INTERPRETABLE DNA TITLE OF INVESTOR. SYMPHETS.	Do 1211 CLOCGO-CT-CT-CCGTC-ACT-CCCGCGGGGGGGGGTGGTGGGGGGGGGG
WINDERS OF SOURCESS: CORRESPONDENCE ADDRESS: ADDRESSEE: TASP MONIQUERY STREET, SALE 2200	1093
CLIFT: San Francisco STATE: California CONTRY: United States of America 77P: 94.10 United States of America	Oy 127 ProHisserprovalLysclutysProvalMetSerAsnIle
COMPUTER REDAMALE ROWS. MEDIUM TYPE: Ploppy disk COMPUTER: LIN PC Comparable OPERATING SYSTEM: CC. DOS MS - DOS	
5. SOUTHARE: Patentin Release #1.0, Version #1.25 CURRENT APELLATION DAYS. SPELICATION NAMES: US_08_V073_394C	161
CLASSIPCACTION 536 PRIOR ADDICATION 376 PRIOR ADDICATION DAW. PLIANS DAYS. 07.795-330	181
ATTORNEY/AGENT INFORMATION: NAME: Oarroll, Peeer G. REASSTRATION NUMBER: 32,837	201 AspGlyAspAsnLeuArgHis
; REFERENCE/DOCKET NUMBER: FORS-00613 ; TELECOMMUNICATION: ; TELECOMONING A15/705-00613	839
TELEPAN 415/700 9410 TELEPAN 415/700 9410 TELEPAN 615/700 9610 EMPIRATE THIRD FOR THE TELEPAN 6110 91	Oy 215 PhelypakleGiuAphrgAtaGiuAphrightaGitArgistis/PallyGiuValAlatysteuPhe  Dp 779 GCGAAGTCCACCAGGGGCAGGTCGGTGGGGCGCCTTGGCCCAGGTCGGAGGTCTTC
LENGTH. 1447 base pays TYPE. molecula from the property of the	Oy 235 AlaAspAlaGlyVallleCystleAlaSerLeulleSerProTyrArgArgAspArgAsp  Db 719 AGATGSTCAAAGAGAACATCTACCOGGAGGAGTTCCAGGAGGAGTTCCAGGAGGAGTTCAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA
~	Oy 255 AlacysArgAlaLeuLeuProHisserAsnPhelleGluValPhelleAsp
All dyment wores: 0.58 Length: 1647 Littlement works: 117.00 Metre 84 Percent similarity: 32.514 Conservative: 21	Oy 272 Leufroleu 274 Db 599 Hintoleu 591

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1333 TGTGGGCCAGGACAGCGGAAAGGGGCCTCTCCACCTCCGGGTAAAGCCAAAGGAGCCTCT 1274
                                                                              1093 CTTCCCTCAGGGCCAGAACGCTCAGGTCTTTGGCGAGAAGCCCCCGCGCGTCCTTCAGGT 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ThrLeuAlaCysAlaLeuSerArgGluLeuH19CysArgGlyH18LeuThrTyrValLeu 200
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                                                                                                                                                                                                                                                                                                                                                        1033 CCCTGAGGGCTTTATAAGGCTCGGGGGCCCGGTGGACCCGGCCCCCCCTGGCGGCGCGCCA 974
                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GlyLysSerThrAsnIleLeuTrpHisAsnCysLeuIleGlyGlnSerAspArgGlnLys 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                             973 GGGCCAGAAGATGGGCCCACATGGGCTCCTTGCGGGAAAGCACAAAGCCCACGAAGGCCC 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                839 CCAAACTCAAGCCTCTCCAAAAAGCCCCAAAAGCTTGCCGGTGGGGTCCCGCCTTTTG 780
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Job time : 74 secs
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                                                                                                 APPLICANT THAILDRESS, ANNES E
APPLICANT TANTHERY, VITCOR I
APPLICANT SHOW, WHICH AND D.
TITLE OF INVENTIORS 5' WICLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTIORS 10M, POLYMERASE
MINIBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CARPACIL, PETER C, RECISERATION NUMBER: 12, 137
REPERBUCE/DOCKET NUMBER: 1508-01000
TELECOMMUNICATION: NUMBER: 1508-0100
TELECOMMUNICATION: (415) 37-05-0101
TELECOM: (415) 37-05-0101
TELECOM CONTROL OF 150 100-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/254,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           Sequence 9, Application US/08254359A
Patent No. 5614402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (qenomic)
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LENGTH: 1647 base pairs
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117.00
32.51%
26.01%
6.41%
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STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                 CALIFORNIA
                                                                                  GENERAL INFORMATION:
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72 -----ValileHisGlyLeuThr 77

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0012-2.406.41_A002 bark Grown 1 (DG1) Sorgham bicolor CRNA, mRNA BESTATOR (1925401)
                                       BG126657 ES9472303

BWG5514 660004H03

BWG5136 HYSMED001

BM407099 ESTSS81426

AW508923 833806. 9

B1300536 88156H02.

B1300536 88156H02.
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Tobase: It of 675)

Cordonnier-Pratt, M.-W., Gingle, A., Marsala.C., Sudman, M. and Pratt
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Sequences have been trimmed to exclude PolyA, vector and regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2502, Athens, GA 30602-7271,
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Contact: Gordonier-Pratt MM
Department of Botany
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AW279147
AV424749
AU132232
AL552855
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Plant Sciences Building, Rm.
Trel: 706 542 1860
Fax: 706 542 1805
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Sorghum bicolor
LOCUS
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SOURCE
ORGANISM
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JOURNAL
COMMENT
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BE357876
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BE355111 DG1_113_B
                                                                                                                                           2, 2002, 01:53:43 ; Search time 1690 Seconds (without alignments) 2739.323 Million cell updates/sec
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                                                                                                                                                                                                                                                        1826
1 RPEHFINOTEPLYTHTQQPP.....PKAMAKQVLCYLEENGYLQA 343
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                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                    nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fotal number of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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gb_9ss:*
em_9ss_hum:*
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em_9ss_pin:*
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, N. and Pratt
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threshold for highest quality sequence
                                                                                                                                                                                    Bukāryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae: PACC
clade; Panicoldees; Andropogoneae; Sordhum.
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impublished (2000)
Context: Condonider-Part MM
Department of Sorder
Pir University of Geograph (2000)
Plant Sciences Building, New 2302, Athens, GA 30602
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Matches:
Conservative:
Mismatches:
Indels:
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High quality sequence start: 23
High quality sequence stop: 682
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below Phred quality 16. The
is 20.
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                                              GI: 9296311
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BE355111.1
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Best Local Similarity:
Query Match:
DB:
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DG1_113_B07.g1_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AspAlaGlyValIleCysIleAlaSerLeuIleSerProTyrArgArgAspAla 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 GlyPheThrGlyIleAspAspProJyrGluProProIleAsnGlyGluIleValIleLys 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 MetLysAspGluGluCysProSerProLysAlaMetAlaLysGlnValLeuCysTyrLeu 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 LeuThrTyrValLeuAspGlyAspAsnLeuArgHisGlyLeuAsnArgAspLeuSerPhe 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysArgAlaLeuLeuProHisSerAsnPheIleGluValPheIleAspLeuProLeuLys 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ATCACGTATGTACTTGATGGTGGCATGCTTAGACATGGCCTCAATGGCTTT
below Phred quality 16. The threshold for highest quality is 20.
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Officials (19.59)

Showmaker, F. (19.59)

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A., Pollie B., Merray, Millier, L., Konhan, T., Merlin, J., Beck, C.,
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                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; 
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                                                                                                                                                                                                                                                                                         AM508923 Innex DST 950 bp mRNA linear ESF 03-DEZ-2001 AM508923 CM = 11030 Glycine max CDNA clone GRNOB SYSTEMS CLONE ID: ACM-S1030 Glycine max CDNA clone GRNOB SYSTEMS CLONE ID: ACM-S1030 Glycine max CDNA clone GRNOB SYSTEMS CLONE ID: ACM-S1030 Glycine Max CDNA CM ST 950 GNN SYSTEMS CLONE ID: MRNA SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlySerGlyLysSerThrLeuAlaCysAlaLeuSerArgGluLeuH1sCysArgGlyH1s 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 GGATCAGGAAAAAGCACGCTTGCATGCTCCCTAGGTAGAGAATTGCAGTCAAGGGGTAAG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 LysalaGluAspArgAlaGluAsnIleArgArgValGlyGluValAlaLysLeuPheAla 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 TCACCAGAAAGCCGGGACTGAGAAATACAGTAGGAACTGCGGAAGTTGCAAATCTTTGCA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 ileCysGluAlaArgAspProLysGlyLeuTyrLysLeuAlaArgThrGlyLysIleLys 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValMetSerAsnIleGlyLysSerThrAsnIleLeuTrpHisAsnCysLeuIleGlyGln
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